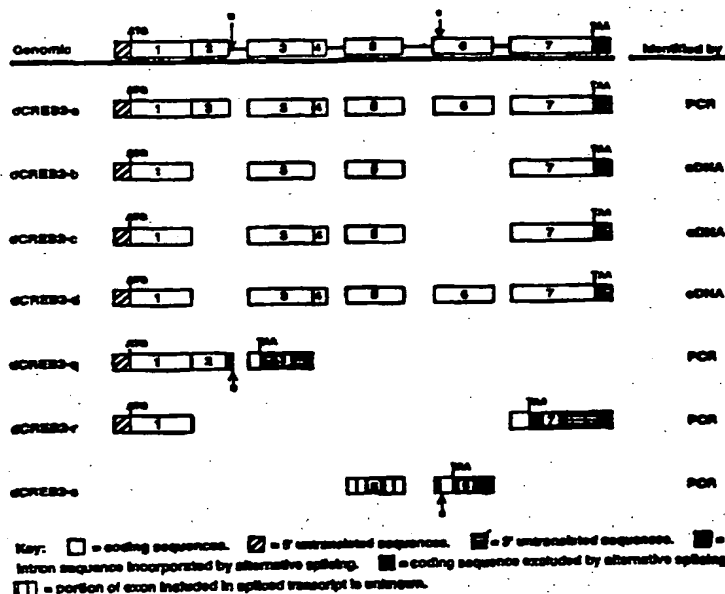




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(54) Title: CLONING AND CHARACTERIZING OF GENES ASSOCIATED WITH LONG-TERM MEMORY



(57) Abstract

A method of regulating long-term memory is disclosed. Also disclosed is isolated DNA encoding a cyclic 3', 5'-adenosine monophosphate responsive transcriptional activator, isolated DNA encoding a' antagonist of cyclic 3', 5'-adenosine monophosphate-inducible transcription, isolated DNA encoding an enhancer-specific activator, and isolated DNA encoding a nitric oxide synthase. A method for assessing the effect of a drug on long-term memory formation is also disclosed.

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CLONING AND CHARACTERIZING OF GENES
ASSOCIATED WITH LONG-TERM MEMORY

Description

Background of the Invention

5 Activation of the cyclic 3',5'-adenosine monophosphate (cAMP) signal transduction pathway can have long-lasting global consequences through its influence on the expression of specific genes. This is true for simple organisms as well as mammals, where many of the known cAMP-responsive
10 genes can have important neural and endocrine roles. Additional information regarding activation of this pathway would be useful, particularly as this activation pertains to the ability of animals to remember activities or events.

Summary of the Invention

15 The present invention is based on Applicants' discovery of the dCREB1 and dCREB2 genes. The present invention is further based on Applicants' discovery that the *Drosophila* CREB2 gene codes for proteins of opposite functions. One isoform (e.g., dCREB2-a) encodes a cyclic
20 3',5'-adenosine monophosphate (cAMP)-responsive transcriptional activator. Another isoform (e.g., dCREB2-b) codes for an antagonist which blocks the activity of the activator.

 When the blocking form is placed under the control of
25 the heat-shock promoter, and transgenic flies are made, a brief shift in temperature induces the synthesis of the blocker in the transgenic fly. This induction of the blocker (also referred to herein as the repressor) specifically disrupts long-term, protein synthesis
30 dependent memory of an odor-avoidance behavioral paradigm.

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As a result of Applicants' discovery, a method is herein provided to regulate long term memory in an animal. The method of regulating long term memory described herein comprises inducing expression of a dCREB2 gene or a
5 fragment thereof in the animal.

The dCREB2 gene encodes several isoforms. Examples of an isoform encoded by the dCREB2 gene are dCREB2-a, dCREB2-b, dCREB2-c, dCREB2-d, dCREB2-q, dCREB2-r and dCREB2-s.

The isoforms encoded by the dCREB2 gene include CAMP-
10 responsive activator isoforms and antagonistic blocker (or repressor) isoforms of the activator isoforms. Cyclic AMP responsive activator isoforms can function as a CAMP-responsive activator of transcription. Antagonistic
15 repressors can act as a blocker of activators. An example of a CAMP-responsive activator isoform is dCREB2-a. An example of an antagonistic repressor (or blocker) isoform is dCREB2-b. The terms blocker and repressor are used interchangeably herein.

In one embodiment of the invention, the dCREB-2 gene
20 encodes a CAMP-responsive activator isoform and inducing said gene results in the potentiation of long term memory.

Alternatively, inducing the dCREB2 gene encoding a CAMP-responsive activator isoform activates the production of a protein which is necessary for the formation of long
25 term memory.

In another embodiment of the invention, the dCREB2 gene encodes a repressor isoform and inducing said gene results in the blocking of long term memory.

A further embodiment of the invention relates to a
30 method of regulating long term memory in an animal comprising inducing repressor and activator isoforms of dCREB2 wherein long term memory is potentiated in the animal when the net amount of functional activator (ΔC) is greater than zero.

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The invention also relates to a method of identifying a substance capable of affecting long term memory in an animal comprising the determination that said substance alters the induction or activity of repressor and activator isoforms of dCREB2 from normal in the animal.

As referred to herein, an activator isoform includes dCREB2-a and functional fragments thereof and a repressor isoform includes dCREB2-b and functional fragments thereof.

Other embodiments of the invention relate to a method of enhancing long term memory formation in an animal comprising increasing the level of activator homodimer from normal, decreasing the level of activator-repressor heterodimer from normal, or decreasing the level of repressor homodimer from normal in the animal.

Still another embodiment of the invention relates to a method of identifying a substance capable of affecting long term memory in an animal comprising the determination that said substance alters activator homodimer, activator-repressor heterodimer and/or repressor homodimer formation from normal in the animal.

As referred to herein, an activator homodimer includes the dCREB2a homodimer, an activator-repressor heterodimer includes the dCREB2a-dCREB2b heterodimer, and a repressor homodimer includes the dCREB2b homodimer.

A further embodiment of the invention relates to isolated DNA encoding a cAMP responsive transcriptional activator. Such a cAMP responsive transcriptional activator can be encoded by a *Drosophila* dCREB2 gene or by homologues or functional fragments thereof. For example, a cAMP responsive transcriptional activator can be encoded by the dCREB2 gene which codes for dCREB2-a or by a gene encoded by the sequences presented herein.

Still another embodiment of the invention relates to isolated DNA encoding an antagonist of cAMP-inducible transcription. Such an antagonist of cAMP-inducible

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transcription can be encoded by a *Drosophila* dCREB2 gene or by homologues or functional fragments thereof. For example, an antagonist of cAMP-inducible transcription can be encoded by the dCREB2 gene which codes for dCREB2-b.

5 Another embodiment of the invention relates to isolated DNA (SEQ ID NO.: 25) which encodes a *Drosophila* dCREB2 gene or functional fragments thereof.

A further embodiment of the invention relates to isolated DNA encoding an enhancer-specific activator. Such
10 an enhancer-specific activator can be encoded by a *Drosophila* dCREB1 gene or by homologues or functional fragments thereof.

Another embodiment of the invention relates to isolated DNA encoding a nitric oxide synthase of *Drosophila*
15 (DNOS). Such DNA can encode a DNOS of neuronal locus. The DNOS encoded can contain, for example, putative heme, calmodulin, flavin mononucleotide (FMN), flavin adenine dinucleotide (FAD) and nicotinamide adenine dinucleotide phosphate, in its reduced form, (NADPH) binding site
20 domains.

A further embodiment of the invention relates to a method for assessing the effect of a drug on long term memory formation comprising administering the drug to *Drosophila*, subjecting the *Drosophila* to classical
25 conditioning to at least one odorant and electrical shock, and assessing the performance index of the classical conditioning, wherein the effect of the drug occurs when it alters the performance index from normal. The drug can affect long term memory formation by, for example, altering
30 the induction or activity of repressor and activator isoforms of dCREB2.

A still further embodiment of the invention relates to the assessment that an animal will have an enhanced or, alternatively, a diminished capability of possessing long
35 term memory. This assessment can be performed by

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determining the amount of cAMP-responsive activator isoforms, cAMP-responsive repressor or blocker isoforms, or dimers of these isoforms that are present in the animal, where these isoforms are encoded by the CREB2 or a homologous gene. Enhanced capability of possessing long term memory will be more likely as the amount of activator exceeds the amount of repressor, i.e. in direct proportion to the size of the net amount of functional activator (ΔC) when this quantity is greater than zero. Conversely, diminished capability of processing long term memory will be more likely as the amount of repressor exceeds the amount of activator, i.e. in direct proportion to the size of the net amount of functional activator (ΔC) when this quantity is less than zero.

Another embodiment of the invention relates to a screening assay of pharmaceutical agents as enhancers of long term memory or as obstructors of long term memory in animals. The screening assay is performed by determining the change in the amount of cAMP-responsive activator isoforms, cAMP-responsive repressor or blocker isoforms, or dimers of these isoforms that is present in an animal or, more preferably, in a cell culture system or in *Drosophila* when the pharmaceutical agent is present, in comparison to when the pharmaceutical agent is not present, where these isoforms are encoded by the CREB2 or a homologous gene. Enhancers of long term memory cause a net increase in the amount of activator isoforms relative to the amount of repressor isoforms, i.e. an increase in the net amount of functional activator (ΔC). Obstructors of long term memory cause a net decrease in the amount of activator isoforms relative to the amount of repressor isoforms, i.e. a decrease in the net amount of functional activator (ΔC). The pharmaceutical agent can cause these changes by acting, for example, to alter the expression (transcription or translation) of the respective activator and/or repressor

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isoforms from the CREB2 or a homologous gene, to alter the formation of activator homodimers, activator-repressor heterodimers and/or repressor homodimers from the expressed isoforms, or to alter the interaction of one or more of these isoform or dimer types at their molecular targets. The long term memory activator isoform/repressor isoform system herein disclosed provides a unique platform for conducting such screening assays.

A further embodiment of the invention relates to an assay of pharmaceutical agents for their property as facilitators or hinderers of long term memory in animals. The assay is performed by administering the pharmaceutical agent to *Drosophila* prior to subjecting the *Drosophila* to a Pavlovian olfactory learning regimen. This regimen assesses the long term memory capabilities of the *Drosophila* by subjecting the flies to a massed and/or a spaced training schedule. Transgenic lines of these flies containing altered dCREB2 genes can be used to further elucidate the long term memory facilitation or hindering property of the pharmaceutical agent. The assay provides data regarding the acquisition of long term memory by the *Drosophila* after exposure to the pharmaceutical agent. These data are compared to long term memory acquisition data from *Drosophila* that have not been exposed to the pharmaceutical agent. If the exposed flies display faster or better retained long term memory acquisition than the unexposed flies, the pharmaceutical agent can be considered to be a facilitator of long term memory. Conversely, if the exposed flies display slower or less retained long term memory acquisition than the unexposed flies, the pharmaceutical agent can be considered to be a hinderer of long term memory. Since the genetic locus for this long term memory assay in *Drosophila* resides in the dCREB2 gene, the results from this assay can be directly applied to

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other animals that have homologous genetic loci (CREB2 or CREM genes).

Brief Description of the Drawings

Figure 1A depicts the DNA sequence (SEQ ID NO.: 1) and predicted amino acid sequence (SEQ ID NO.: 2) of the dCREB2-a coding region. The basic region and leucine zipper domains are indicated by solid and broken bold underlining, respectively; positively-charged residues in the basic region are circled; periodic leucines in the zipper motif are boxed; glutamines in the activation domain are underlined; the short amino acid motif with target sites for kinases, starting at residue 227, is indicated by a bold outline; and sequences specified by alternatively-spliced exons 2, 4 and 6 are shaded.

Figure 1B depicts the amino acid sequences of the bZIP domains of dCREB2 (SEQ ID NO.: 3), mammalian CREB (SEQ ID NO.: 4), CREM (SEQ ID NO.: 5) and ATF-1 (SEQ ID NO.: 6). Differences between dCREB2 and CREB are boxed.

Figure 2 is a schematic diagram of dCREB2 isoforms with the exon boundaries defined with respect to dCREB2-a. Diagram is not drawn to scale.

Figure 3 is a bar graph representation of results showing pKA-responsive transcriptional activation by dCREB2-a.

Figure 4 is a bar graph representation of results showing the transcriptional effect of dCREB2-b and a mutant variant on pKA-responsive activation by dCREB2-a.

Figure 5 depicts the DNA sequence (SEQ ID NO.: 7) and predicted amino acid sequence (SEQ ID NO.: 8) of the dCREB1 coding region. The basic region and leucine zipper domains are indicated by solid and broken bold underlining, respectively; positively-charged residues in the basic region are circled; periodic leucines of the zipper motif are boxed; and in the acid-rich region of the activation

domain, negatively-charged amino acids are underlined and proline residues are indicated by diamonds.

Figure 6 is a bar graph representation of results showing transcriptional activation of a CRE reporter gene by *dCREB1* in *Drosophila* Schneider L2 cell culture.

Figure 7A is a photomicrograph of a Northern blot depicting the effect of heat shock induction on *dCREB2-b* expression: wt = wildtype flies; CREB = 17-2 transgenic flies; lanes 1-2: no heat shock; lanes 2-3: immediately after heat shock; lanes 5-6: three hours after heat shock.

Figure 7B is a photograph of a Western blot depicting the effect of heat shock induction on *dCREB2-b* protein production: wt = wildtype flies; CREB = 17-2 transgenic flies; lanes 1-2: no heat shock; lanes 2-3: immediately after heat shock; lanes 5-6: one hour after heat shock; lanes 7-8: three hours after heat shock; lanes 9-10: 9 hours after heat shock; lanes 11-12: 24 hours after heat shock.

Figure 7C is a photograph of a Western blot depicting the effect of heat shock induction on *dCREB2* and *dCREB2-mLZ* (a mutated *dCREB2-b*) protein production: wt = 17-2 transgenic flies (expressing wildtype blocker, *dCREB2-b*); m = A2-2 transgenic flies (expressing mutant blocker, *dCREB2-mLZ*); lanes 1-2: no heat shock; lanes 3-4: immediately after heat shock; lanes 5-6: three hours after heat shock; lanes 7-8: six hours after heat shock.

Figure 8 is a bar graph representation of results showing the effect of cycloheximide (CXM) feeding, before or after spaced or massed training, on one-day memory retention: stripped bars = +CXM; hatched bars = -CXM.

Figure 9A is a bar graph representation of results showing the effect of heat shock induction on one-day memory retention in wildtype (Can-S) flies and *hs-dCREB2-b* transgenic (17-2) flies given spaced or massed training:

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hatched bars = wildtype (Can-S) flies; stripped bars: *hs-dCREB2-b* transgenic (17-2) flies; *hs* = heat shock.

Figure 9B is a bar graph representation of results showing the effect of heat shock induction on one-day
5 memory retention in wildtype (Can-S) flies or *hs-dCREB2-b* transgenic (M11-1) flies given spaced or massed training: hatched bars = wildtype (Can-S) flies; stripped bars: *hs-dCREB2-b* transgenic (M11-1) flies; *hs* = heat shock.

Figure 9C is a bar graph representation of results
10 showing the effect of heat shock induction on learning in wildtype (Can-S) flies and *hs-dCREB2-b* transgenic (17-2) flies given spaced or massed training: hatched bars = wildtype (Can-S) flies; stripped bars: *hs-dCREB2-b* transgenic (17-2) flies; *hs* = heat shock.

Figure 10 is a bar graph representation of results
15 showing the effect of heat shock induction on one-day memory retention in wildtype [*w(isoCJ1)*] flies, *hs-dCREB2-b* transgenic (17-2) flies, and mutant *hs-dCREB2-mLZ* transgenic (A2-2) flies given spaced training: hatched bars
20 = wildtype [*w(isoCJ1)*] flies; stripped bars = *hs-dCREB2-b* transgenic (17-2) flies; white bars = mutant *hs-dCREB2-mLZ* transgenic (A2-2) flies; *hs* = heat shock.

Figure 11 is a bar graph representation of results
25 showing the effect of heat shock induction on seven-day memory retention (long term memory) in wildtype (Can-S) flies and *hs-dCREB2-b* transgenic (17-2) flies given spaced training: hatched bars = wildtype (Can-S) flies; stripped bars = *hs-dCREB2-b* transgenic (17-2) flies; *hs* = heat shock.

Figure 12 is a bar graph representation of results
30 showing the effect of heat shock induction on one-day memory retention in *hs-dCREB2-b* transgenic (17-2) flies, *radish* mutant flies, and *radish hs-dCREB2-b* double mutant (*rsh;17-2*) flies given spaced training: *hs* = heat shock;
35 hatched bars = -*hs*; stripped bars = +*hs*.

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Figure 13A is a graphic representation of results showing the effect of repeated training sessions on seven-day memory retention (long term memory) in wildtype (Can-S) flies with long term memory as a function of the number of training sessions indicated by open circles and a negative accelerating exponential Gompertz (growth) function fit to the individual performance indexes (PIs) using a nonlinear iterative least squares method indicated by the solid line.

Figure 13B is a graphic representation of results showing the effect of the rest interval between each training session on seven-day memory retention (long term memory) in wildtype (Can-S) flies with long term memory as a function of the rest interval indicated by open circles and a negative accelerating exponential Gompertz (growth) function fit to the individual performance indexes (PIs) using a nonlinear iterative least squares method indicated by the solid line.

Figure 14 depicts a conceptual model of a molecular switch for the formation of long term memory based on differential regulation of CREB isoforms with opposing functions with ΔC indicating the net effect of CREB activators.

Figure 15A is a bar graph representation of results showing the effect of 48 massed training sessions (48x massed) or 10 spaced training sessions with a 15-minute rest interval (10x spaced) on seven-day memory retention in wildtype (Can-S) flies.

Figure 15B is a bar graph representation of results showing the effect of one (1x), two (2x) or ten (10x) massed training sessions, three hours after heat-shock induction of the transgene (induced) or in the absence of heat-shock (uninduced), on seven-day memory retention in wildtype (Can-S) flies, *hsp-dCREB2-a* transgenic (C28) flies, and *hsp-dCREB2-a* transgenic (C30) flies: black bars = wildtype (Can-S) flies; stripped bars = *hsp-dCREB2-a*

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transgenic (C28) flies; and white bars = *hsp-dCREB2-a* transgenic (C30) flies.

Figure 15C is a bar graph representation of results showing responses three hours after heat shock in wildtype (Can-S) flies and *hsp-dCREB2-a* transgenic (C28) flies to odors, either octanol (OCT) or methylcyclohexanol (MCH), or to shock (60 V DC): black bars = wildtype (Can-S) flies; stripped bars = *hsp-dCREB2-a* transgenic (C28) flies.

Figure 16A-16C depict the deduced amino acid sequences of DNOS and mammalian NOSs with amino acid numbering starting at the first methionine in each open reading frame (ORF), putative binding domains for cofactors (overlined) demarcated as in previously published reports on mammalian NOSs, and amino acids which have been proposed as contacts with FAD and NADPH based on crystal structure of the ferredoxin NADP⁺ reductase (Karpus, P.A., *Science*, 251: 60-66 (1991)) conserved at equivalent positions (bullet points): DNOS, *Drosophila* NOS (SEQ ID NO.: 9); RNNOS, rat neuronal NOS (SEQ ID NO.: 10); BENOS, bovine endothelial NOS (SEQ ID NO.: 11); MMNOS, mouse macrophage NOS (SEQ ID NO.: 12). Sequence alignment and secondary structure predictions were performed by Geneworks 2.3 (IntelliGenetics).

Figure 16D is a schematic diagram of the domain structure of *Drosophila* and mammalian NOS proteins with the proposed cofactor-binding sites for heme (H), calmodulin (CaM), flavin mononucleotide (FMN), flavin adenine dinucleotide (FAD), nicotinamide adenine dinucleotide phosphate (NADPH) and the glutamine-rich domain (Q) in DNOS shown.

Figure 17A is a photograph of a Western blot showing DNOS expression in 293 human embryonic kidney cells.

Figure 17B is a bar graph representation of results showing DNOS enzyme activity measured in 293 human embryonic kidney cell extracts by conversion of ³H-L-

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arginine to ^3H -L-citrulline: in the presence of exogenous Ca^{2+} or calmodulin (group B); in the presence of 1 mM EGTA without exogenous Ca^{2+} or calmodulin (group C); in the presence of 100 mM L-NAME with exogenous Ca^{2+} or calmodulin (group D).

Figure 18A is a photomicrograph of a Northern blot showing a 5.0 kb dNOS transcript present in *Drosophila* heads: H = head; B = body.

Figure 18B is a photograph of an agarose gel stained with ethidium bromide showing the expression by the dNOS gene of two alternatively spliced mRNA species with the arrows indicating the positions of the DNA fragments of the expected sizes: the 444 bp long-form fragment and the 129 bp short-form fragment. The other bands present in the lane are artifacts from heteroduplexes that failed to denature. KB = size markers.

Figure 18C depicts the alignment of the deduced amino acid sequence of two protein isoforms of DNOS and mouse neuronal NOS: top part shows the relation between two conceptual *Drosophila* NOS proteins, DNOS-1 (amino acid residues 408-427 and 513-532 of SEQ ID NO.: 9) and DNOS-2 (SEQ ID NO.: 14), corresponding to the longer and shorter RT-PCR products, respectively; the bottom part shows the relationship between the relevant regions of two protein isoforms of the mouse neuronal NOS, n-NOS-1 (amino acid residues 494-513 and 599-618; SEQ ID NO.: 13 and SEQ ID NO.: 15, respectively) and n-NOS-2 (SEQ ID NO.: 16); and the numbers indicate the positions of the amino acid residues relative to the first methionine in the respective ORFs.

Figure 19A-19B depicts the nucleotide sequence (SEQ ID NO.: 25) of a dNOS cDNA encoding the DNOS protein. The open reading frame of 4050 bp starts at nucleotide 189 and ends at nucleotide 4248.

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Detailed Description of the Invention

Applicants have cloned and characterized two genes, designated dCREB2 and dCREB1, isolated through a DNA-binding expression screen of a *Drosophila* head cDNA library in which a probe containing three cAMP-responsive element (CRE) sites was used.

The dCREB2 gene codes for the first known cAMP-dependent protein kinase (PKA) responsive CREB/ATF transcriptional activator in *Drosophila*. A protein data base search showed mammalian CREB, CREM and ATF-1 gene products as homologous to dCREB2. For these reasons, dCREB2 is considered to be a member, not only of the CREB/ATF family, but of the specific cAMP-responsive CREB/CREM/ATF-1 subfamily. It is reasonable to expect that dCREB2 is involved in *Drosophila* processes which are analogous to those which are thought to depend on cAMP-responsive transcriptional activation in other animal systems.

Applicants have shown that the dCREB2 transcript undergoes alternative splicing. Splice products of dCREB2 were found to fall into two broad categories: one class of transcripts (dCREB2-a, -b, -c, -d) which employs alternative splicing of exons 2, 4 and 6 to produce isoforms whose protein products all have the bZIP domains attached to different versions of the activation domain and a second class of transcripts (dCREB2-q, -r, -s) which have splice sites which result in in-frame stop codons at various positions upstream of the bZIP domain. These all predict truncated activation domains without dimerization or DNA binary activity.

dCREB2-a, -b, -c and -d are splice forms that predict variants of the activation domain attached to a common basic region-leucine zipper. These alternative splice forms result in seemingly minor changes in the size and spacing of parts of the activation domain. Nevertheless,

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alternative splicing of the activation domain has profound effects on the functional properties of dCREB2 products. Isoform dCREB2-a produces a PKA-responsive transcriptional activator in cell culture, whereas dCREB2-b, lacking exons
5 2 and 6, produces a specific antagonist. This dCREB2 splicing pattern (and its functional consequences) is virtually identical to that seen in the CREM gene. Similarly located, alternatively-spliced exons in the CREM gene determine whether a particular isoform is an activator
10 or an antagonist (deGroot, R.P. and P. Sassone-Corsi, *Mol. Endocrinol.*, 7: 145-153 (1993); Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)).

The ability of the phosphorylation domain (KID domain) to activate in trans other constitutive transcription
15 factors which are bound nearby could potentially transform a CREM antagonist (which contains the KID domain but is lacking an exon needed for activation) into a cAMP-responsive activator. Since the modular organization of these molecules has been conserved, dCREB2-d could have
20 this property.

In contrast to the dCREB2 splicing variants that encode isoforms with a basic region-leucine zipper domain, the dCREB2-q, -r and -s splice forms incorporate in-frame stop codons whose predicted protein products are truncated
25 before the bZIP region. Isoforms of this type have been identified among the products of the CREB gene (deGroot, R.P. and P. Sassone-Corsi, *Mol. Endocrinol.*, 7: 145-153 (1993); Ruppert, S. et al., *EMBO J.*, 11: 1503-1512 (1992)) but not the CREM gene. The function of these truncated
30 CREB molecules is not known, but at least one such CREB mRNA is cyclically regulated in rat spermatogenesis (Waeber, G. et al., *Mol. Endocrinol.*, 5: 1418-1430 (1991)).

So far, dCREB2 is the only cAMP-responsive CREB transcription factor isolated from *Drosophila*. Other
35 *Drosophila* CREB molecules, BBF-2/dCREB-A (Abel, T. et al.,

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Genes Dev., 6: 466-488 (1992); Smolik, S.M. et al., Mol. Cell Biol., 12: 4123-4131 (1992)), dCREB-B (Usui, T. et al., DNA and Cell Biology, 12(7): 589-595 (1993)) and dCREB1, have less homology to mammalian CREB and CREM. It may be that dCREB2 subsumes functions of both the CREB and CREM genes in *Drosophila*. The mammalian CREB and CREM genes are remarkably similar to one another in several respects. It has been suggested that CREB and CREM are the product of a gene duplication event (Liu, F. et al., J. Biol. Chem., 268: 6714-6720 (1993); Riabowol, K.T. et al., Cold Spring Harbor Symp. Quant. Biol., 1: 85-90 (1988)). dCREB2 has a striking degree of amino acid sequence similarity to the CREB and CREM genes in the bZIP domain. Moreover, comparison of alternative splicing patterns among CREB, CREM and dCREB2 indicates that dCREB2 generates mRNA splicing isoforms similar to exclusive products of both CREB and CREM. Taken together, the sequence information and the splicing organization suggest that dCREB2 is an ancestor of both the mammalian CREB and CREM genes.

As discussed further herein, one phenomenon in which dCREB2 might act with enduring consequences is in long-term memory. This possibility is a particularly tempting one because recent work in *Aplysia* indicates that a CREB factor is likely to function in long-term facilitation by inducing an "immediate early" gene (Alberini, C.M. et al., Cell, 76: 1099-1114 (1994); Dash, P.K., Nature, 345: 718-721 (1990)). Recent experiments with a conditionally-expressed dCREB2-b transgene indicate that it has specific effects on long-term memory in *Drosophila*.

The product of the second gene described herein, dCREB1, also appears to be a member of the CREB/ATF family. Gel-retardation assays indicate that it binds specifically to CREs. It has a basic region and an adjacent leucine zipper at its carboxyl end, but this domain shows limited amino acid sequence similarity to other CREB/ATF genes.

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The presumed transcriptional activation domain of dCREB1 is of the acid-rich variety. Furthermore, it has no consensus phosphorylation site for PKA. dCREB1 can mediate transcriptional activation from CRE-containing reporters in the *Drosophila* L2 cell line, but this activation is not dependent on PKA.

A recurrent finding from work on the biology of learning and memory is the central involvement of the cAMP signal transduction pathway. In *Aplysia*, the cAMP second-messenger system is critically involved in neural events underlying both associative and non-associative modulation of a behavioral reflex (Kandel, E.R. and J.H. Schwartz, *Science*, 218: 433-443 (1982); Kandel, E.R., et al., In *Synaptic Function*, Edelman, G.M., et al. (Eds.), John Wiley and Sons, New York (1987); Byrne, J.H., et al., In *Advances in Second Messenger and Phosphoprotein Research*, Shenolikar, S. and A.C. Nairn (Eds.), Raven Press, New York, pp. 47-107 (1993)). In *Drosophila*, two mutants, *dunce* and *rutabaga*, were isolated in a behavioral screen for defects in associative learning and are lesioned in genes directly involved in cAMP metabolism (Quinn, W.G., et al., *Proc. Natl. Acad. Sci. USA*, 71: 708-712 (1974); Dudai, Y., et al., *Proc. Natl. Acad. Sci., USA* 73: 1684-1688 (1976); Byers, D. et al., *Nature*, 289: 79-81 (1981); Livingstone, M.S., et al., *Cell*, 37: 205-215 (1984); Chen, C.N. et al., *Proc. Natl. Acad. Sci. USA*, 83: 9313-9317 (1986); Levin, L.R., et al., *Cell*, 68: 479-489 (1992)). These latter observations were extended with a reverse-genetic approach using inducible transgenes expressing peptide inhibitors of cAMP-dependent protein kinase (PKA) and with analyses of mutants in the PKA catalytic subunit (Drain, P. et al., *Neuron*, 6: 71-82 (1991); Skoulakis, E.M., et al., *Neuron*, 11: 197-208 (1993)). Recent work on mammalian long-term potentiation (LTP) also has indicated a role for cAMP in synaptic

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plasticity (Frey, U., et al., *Science*, 260: 1661-1664 (1993); Huang, Y.Y. and E.R. Kandel, In *Learning and Memory*, vol. 1, pp.74-82, Cold Spring Harbor Press, Cold Spring Harbor, NY (1994)).

5 The formation of long-lasting memory in animals and of long-term facilitation in *Aplysia* can be disrupted by drugs that interfere with transcription or translation (Agranoff, B.W. et al., *Brain Res.*, 1: 303-309 (1966); Barondes, S.H. and H.D. Cohen, *Nature*, 218: 271-273 (1968); Davis, H.P. and L.R. Squire, *Psychol. Bull.*, 96: 518-559 (1984);
10 Rosenzweig, M.R. and E.L. Bennett, In *Neurobiology of Learning and Memory*, Lynch, G., et al. (Eds.), The Guilford Press, New York, pp. 263-288, (1984); Montarolo, P.G., et al., *Science*, 234: 1249-1254 (1986)). This suggests that
15 memory consolidation requires *de novo* gene expression. Considered along with the involvement of the cAMP second-messenger pathway, this requirement for newly synthesized gene products suggests a role for cAMP-dependent gene expression in long-term memory (LTM)
20 formation.

 In mammals, a subset of genes from the CREB/ATF family are known to mediate cAMP-responsive transcription (Habener, J.F., *Mol. Endocrinol.*, 4: 1087-1094 (1990); deGroot, R.P. and P. Sassone-Corsi, *Mol. Endocrinol.*, 7:
25 145-153 (1993)). CREBs are members of the basic region-leucine zipper transcription factor superfamily; (Landschulz, W.H. et al., *Science*, 240: 1759-1764 (1988)). The leucine zipper domain mediates selective homo- and hetero-dimer formation among family members (Hai, T.Y. et
30 al., *Genes & Dev.*, 3: 2083-2090 (1989); Hai, T. and T. Curran, *Proc. Natl. Acad. Sci. USA*, 88: 3720-3724 (1991)). CREB dimers bind to a conserved enhancer element (CRE) found in the upstream control region of many cAMP-responsive mammalian genes (Yamamoto, K.K., et al.,
35 *Nature*, 334: 494-498 (1988)). Some CREBs become

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transcriptional activators when specifically phosphorylated by PKA (Gonzalez, G.A. and M.R. Montminy, *Cell*, 59: 675-680 (1989); Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)), while others, isoforms from the CREM gene, are functional antagonists of these PKA-responsive activators (Foulkes, N.S. et al., *Cell*, 64: 739-749 (1991); Foulkes, N. and P. Sassone-Corsi, *Cell*, 68: 411-414 (1992)).

Work in *Aplysia* has shown that cAMP-responsive transcription is involved in long-term synaptic plasticity (Schacher, S. et al., *Science*, 240: 1667-1669 (1988); Dash, P.K., *Nature*, 345: 718-721 (1990)). A primary neuronal co-culture system has been used to study facilitation of synaptic transmission between sensory and motor neurons comprising the monosynaptic component of the *Aplysia* gill-withdrawal reflex. Injection of oligonucleotides containing CRE sites into the nucleus of the sensory neuron specifically blocked long-term facilitation (Dash, P.K., *Nature*, 345: 718-721 (1990)). This result suggests that titration of CREB activity might disrupt long-term synaptic plasticity.

Described herein is the cloning and characterization of a *Drosophila* CREB gene, dCREB2. This gene produces several isoforms that share overall structural homology and nearly complete amino acid identity in the basic region-leucine zipper with mammalian CREBs. The dCREB2-a isoform is a PKA-responsive transcriptional activator whereas the dCREB2-b product blocks PKA-responsive transcription by dCREB2-a in cell culture. These molecules with opposing activities are similar in function to isoforms of the mammalian CREM gene (Foulkes, N.S. et al., *Cell*, 64: 739-749 (1991); Foulkes, N. and P. Sassone-Corsi, *Cell*, 68: 411-414 (1992); Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)). The numerous similarities in sequence and function between dCREB2 and mammalian CREBs suggest

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that cAMP-responsive transcription is evolutionarily conserved.

Genetic studies of memory formation in *Drosophila* have revealed that the formation of a protein synthesis-
5 dependent long-term memory (LTM) requires multiple training sessions with a rest interval between them. As discussed further herein, this LTM is blocked specifically by induced expression of a repressor isoform of the cAMP-responsive transcription factor CREB. Also as discussed further
10 herein, LTM information is enhanced after induced expression of an activator form of CREB. Maximum LTM is achieved after just one training session.

To investigate the role of CREBs in long-term memory (LTM) formation in *Drosophila*, dominant-negative transgenic
15 lines which express *dCREB2-b* under the control of a heat-shock promoter (*hs-dCREB2-b*) were generated. Groups of flies, which had been heat-shock induced or left uninduced, were tested for memory retention after Pavlovian olfactory learning. This acute induction regimen minimized
20 potential complications from inappropriate expression of *dCREB2-b* during development and allowed a clear assessment of the effect of *hs-dCREB2-b* induction on memory formation.

In *Drosophila*, consolidated memory after olfactory learning is composed of two genetically distinct
25 components: anesthesia-resistant memory (ARM) and long-term memory (LTM). ARM decays to zero within four days after training, and formation of ARM is insensitive to the protein synthesis inhibitor cycloheximide (CXM) but is disrupted by the *radish* mutation (Folkers, E., et al.,
30 *Proc. Natl. Acad. Sci. USA*, 90: 8123-8127 (1993)). In contrast, LTM shows essentially no decay over at least seven days, its formation is cycloheximide-sensitive and it is not disrupted by *radish*. Two different training protocols involving massed and spaced sessions were
35 employed (Ebbinghaus, H., *Über das Gedächtnis*, Dover, New

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York (1885); Baddeley, A.D., *The Psychology of Memory*, Basic Books, New York (1976)) to dissect memory formation. The massed training procedure consists of ten consecutive training cycles with no rest interval between them, while
5 the spaced training protocol consists of the same number of sessions but with a 15-minute rest between each. Their genetic dissection revealed that the massed protocol produced only ARM, while the spaced protocol produced memory retention composed of both ARM and LTM.

10 The behavioral results show that formation of LTM is completely blocked by induced expression of hs-dCREB2-b. This effect is remarkable in its behavioral specificity. ARM, a form of consolidated memory genetically distinguishable from LTM, but co-existing with it one-day
15 after spaced training, was not affected. Learning and peripheral behaviors likewise were normal. Thus, the effect of the induced hs-dCREB2-b transgene is specific to LTM.

Induction of the mutant blocker did not affect LTM.
20 This result, together with the molecular data which showed that induction of the wild-type blocker did not have widespread effects on transcription, suggests that the blocker is reasonably specific at the molecular level when it specifically blocks LTM. The wild-type blocker may
25 disrupt cAMP-dependent transcription *in vivo*, since it can block cAMP-responsive transcription in cell culture. It is reasonable to infer that dimerization is necessary for blocker function and that the wild-type blocker could interfere with cAMP-responsive transcription either by
30 forming heterodimers with dCREB2-a, the activator, or by forming homodimers and competing for DNA binding with homodimers of dCREB2-a. Thus, activators and repressors may form homodimers or heterodimers. It is reasonable to infer that long term memory is enhanced when the level of
35 activator homodimer is increased from normal and/or when

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the level of activator-repressor heterodimer is decreased from normal and/or when the level of repressor homodimer is decreased from normal. In any case, the molecular target(s) of dCREB2-b are likely to be interesting because
5 of the behavioral specificity of the block of LTM.

In *Drosophila*, consolidation of memory into long-lasting forms is subject to disruption by various agents. A single-gene mutation *radish* and the pharmacological agent CXM were used to show that long-lasting memory in flies is
10 dissectable into two components, a CXM-insensitive ARM, which is disrupted by *radish*, and a CXM-sensitive LTM, which is normal in *radish* mutants. As described herein, CREB-family members are likely to be involved in the CXM-sensitive, LTM branch of memory consolidation. The results
15 described herein, taken together with the showing that long-term memory is dissectable into a CXM-insensitive ARM and a CXM-sensitive LTM, show that only one functional component of consolidated memory after olfactory learning lasts longer than four days, requires *de novo* protein
20 synthesis and involves CREB-family members.

Based on work in *Aplysia*, a model has been proposed to describe the molecular mechanism(s) underlying the transition from short-term, protein synthesis-independent to long-term, protein synthesis-dependent synaptic
25 plasticity (Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994)). The present work in *Drosophila* on long-term memory extends this model to the whole organism. Important molecular aspects of this transition seem to involve migration of the catalytic subunit of PKA into the nucleus
30 (Backsai, B.J. et al., *Science*, 260: 222-226 (1993)) and subsequent phosphorylation and activation of CREB-family members (Dash, P.K., *Nature*, 345: 718-721 (1990); Kaang, B.K., et al., *Neuron*, 10: 427-435 (1993)). In flies, it is likely that the endogenous dCREB2-a isoform is one of these
35 nuclear targets. Activated dCREB2-a molecules then might

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transcribe other target genes, including the immediate early genes--as is apparently the case in *Aplysia*. (Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994)).

It is remarkable that the cAMP signal transduction pathway, including its nuclear components, seem to be required for memory-related functions in each of these species and behavioral tasks. Taken together with cellular analyses of a long-lasting form of LTP in hippocampal slices (Frey, U., et al., *Science*, 260: 1661-1664 (1993); Huang, Y.Y. and E.R. Kandel, In *Learning and Memory*, vol. 1, pp.74-82, Cold Spring Harbor Press, Cold Spring Harbor, NY (1994)), the emerging picture is that cAMP-responsive transcription is a conserved molecular switch involved in the consolidation of short-term memory to long-term memory. Thus, it is reasonable to infer that differential regulation of CREB isoforms serves as a molecular switch for the formation of long term memory.

A universal property of memory formation is that spaced training (repeated training sessions with a rest interval between them) produces stronger, longer-lasting memory than massed training (the same number of training sessions with no rest interval) (Ebbinghaus, H., *Uber das Gedachtnis*, Dover, New York (1885); Hintzman, D.L., In *Theories in Cognitive Psychology: The Loyola Symposium*, R.L. Solso (Ed.), pp. 77-99, Lawrence Erlbaum Assoc., Hillsdale, New Jersey (1974); Carew, T.J., et al., *Science*, 175: 451-454 (1972); Frost, W.N., et al., *Proc. Natl. Acad. Sci. USA*, 82: 8266-8269 (1985)). This phenomenon also exists in fruit flies for a conditioned odor avoidance response (Tully, T. and W.G. Quinn, *J. Comp. Physiol.* 157: 263-277 (1985)). Genetic dissection of this long-lasting memory has revealed, however, an important difference between massed and spaced training. Spaced training produces two functionally independent forms of consolidated

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memory, ARM and LTM, while massed training produces only ARM.

As described herein, ARM and LTM differ primarily in their requirement for protein synthesis during induction.

5 ARM is not affected when flies are fed the protein synthesis inhibitor cycloheximide (CXM) immediately before or after training, while LTM is completely blocked under the same feeding conditions. ARM in normal flies also decays away within four days after training, while LTM

10 shows no decay for at least seven days. Thus, protein synthesis is required to induce LTM, but LTM is maintained indefinitely once formed. These latter properties of LTM have been observed throughout the animal kingdom (Davis, H.P. and L.R. Squire, *Psychol. Bull.*, 96: 518-559 (1984);

15 Castellucci, V.F., et al., *J. Neurobiol.*, 20: 1-9 (1989); Erber, J., *J. Comp. Physiol. Psychol.*, 90: 41-46 (1976); Jaffe, K., *Physiol. Behav.*, 25: 367-371 (1980)). The emerging neurobiological interpretation is that formation of LTM involves protein synthesis-dependent structural

20 changes at relevant synapses (Greenough, W.T., *TINS*, 7: 229-283 (1984); Buonomano, D.V. and J.H. Byrne, *Science*, 249: 420-423 (1990); Nazif, F.A., et al., *Brain Res.*, 539: 324-327 (1991); Stewart, M.G., *In Neural and Behavioural Plasticity: The Use of the Domestic Chick As A Model*, R.J. Andrew (Ed.), pp. 305-328, Oxford, Oxford (1991); Bailey, C.H. and E.R. Kandel, *Sem. Neurosci.*, 6:35-44 (1994)). The modern molecular view is that regulation of gene expression underlies this protein synthesis-dependent effect (Goellet, P. et al., *Nature*, 322: 419-422 (1986); Gall, C.M. and J.C. Lauterborn, *In Memory: Organization and Locus of Change*, L.R. Squire, et al., (Eds.) pp.301-329 (1991); Armstrong, R.C. and M.R. Montminy, *Annu. Rev. Neurosci.*, 16: 17-29 (1993)).

Why is spaced training required to induce LTM? The

35 massed and spaced procedures both entail ten training

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sessions; consequently, flies receive equivalent exposure to the relevant stimuli (one odor temporally paired with electric shock and a second odor presented without shock). The only procedural difference between massed and spaced training is the rest interval between each training session. The absence of a rest interval between sessions during massed training does not appear to disrupt the memory formation process. The level of initial learning assayed immediately after massed training is similar to that after spaced training. In addition, ARM levels are similar after both training procedures. Thus, the presence of a rest interval during spaced training seems crucial to the induction of LTM.

To investigate the temporal kinetics of this rest interval in relation to the formation of LTM (Figures 13A and 13B), it was first established that the usual ten sessions of spaced training produced maximal 7-day memory retention (7-day retention is composed solely of LTM, since ARM decays to zero within four days).

Figure 13A shows that 15 or 20 training sessions did not improve memory retention. Thus, ten spaced training sessions produces maximal, asymptotic levels of LTM.

LTM as a function of the length of the rest interval between 10 spaced training sessions was then assessed. Figure 13B reveals a continuous increase in LTM from a 0-min rest interval (massed training) to a 10-minute rest interval, at which time LTM levels reach maximum. Longer rest intervals yielded similar memory scores. These observations of LTM formation suggest an underlying biological process, which changes quantitatively during the rest interval between sessions and which accumulates over repeated training sessions.

In transgenic flies, the formation of LTM, but not ARM or any other aspect of learning or memory, is disrupted by induced expression of a repressor form of the cAMP-

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responsive transcription factor CREB (Example 4). Mutating two amino acids in the "leucine zipper" dimerization domain of this CREB repressor was sufficient to prevent the dominant-negative effect on LTM. Thus, indication of LTM is not only protein synthesis-dependent but also is CREB-dependent. Stated more generally, CREB function is involved specifically in a form of a memory that is induced only by spaced training. This observation was particularly intriguing in light of the molecular nature of CREB.

10 In *Drosophila*, transcriptional and/or post-translational regulation of dCREB2 yields several mRNA isoforms. Transient transfection assays in mammalian F9 cells have demonstrated that one of these isoforms (CREB2-a) functions as a cAMP-responsive activator of transcrip-
15 tion, while a second isoform (CREB2-b) acts as an antagonistic repressor of the activator (Example 1; cf. Habener, J.F., *Mol. Endocrinol.*, 4: 1087-1094 (1990); Foulkes, N. and P. Sassone-Corsi, *Cell*, 68: 411-414 (1992)). (This repressor isoform was used previously to
20 generate the inducible transgene mentioned above.) The existence of different CREB isoforms with opposing functions suggested an explanation for the requirement of multiple training sessions with a rest interval between them for the formation of LTM.

25 In its simplest form, this model (Example 7; Figure 14) supposes that cAMP-dependent protein kinase (PKA), activated during training, induces the synthesis and/or function of both CREB activator and repressor isoforms (cf. Yamamoto, K.K., et al., *Nature*, 334: 494-498 (1988);
30 Backsai, B.J. et al., *Science*, 260: 222-226 (1993)). Immediately after training, enough CREB repressor exists to block the ability of CREB activator to induce downstream events. Then, CREB repressor isoforms are inactivated faster than CREB activator isoforms. In this manner, the
35 net amount of functional activator ($\Delta C = \text{CREB2a} - \text{CREB2b}$)

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increases during a rest interval and then accumulates over repeated training sessions (with a rest interval) to induce further the downstream targets involved with the formation of LTM (Montarolo, P.G., et al., *Science*, 234: 1249-1254
5 (1986); Kaang, B.K., et al., *Neuron*, 10: 427-435 (1993)).

This model leads to three predictions, which have been confirmed. First, if the functional difference between CREB activator and repressor isoforms is zero ($\Delta C=0$) immediately after one training session, then additional
10 massed training sessions should never yield LTM. Figure 15A shows that 48 massed training sessions, rather than the usual 10, still does not produce any 7-day memory retention. Second, if the amount of CREB repressor is increased experimentally, ΔC will be negative immediately
15 after training ($\Delta C < 0$). Then, enough CREB repressor may not decay during a rest interval to free enough CREB activator for induction of LTM. This has been shown to be the case for spaced training (15-min rest interval) after inducing the expression of a *hsp-dCREB2-b* (repressor)
20 transgene three hours before training (Example 4). Third, if the amount of CREB activator is increased experimentally, ΔC will be positive immediately after training ($\Delta C > 0$). This effect, then, should eliminate or reduce the rest interval required to induce LTM. Figure
25 15B shows the results from recent experiments in which the expression of a *hsp-dCREB2-a* (activator) transgene was induced three hours before training. In these transgenic flies, massed training produced maximal LTM. This effect appeared not to arise trivially, since olfactory acuity,
30 shock reactivity (Figure 15C) and initial learning were normal in transgenic flies after heat shock-induction. Thus, the requirement for a rest interval between training sessions to induce LTM specifically was eliminated.

Figure 15B also shows that maximal LTM occurred in
35 induced *hsp-dCREB2-a* transgenic flies after just one

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training session. The usual requirement for additional training to form a strong, long-lasting memory was no longer necessary. Thus, induced overexpression of a CREB activator has produced in otherwise normal flies, the functional equivalent of a "photographic" memory. This result indicates that the amount of CREB activator present during training -- rather than the amount of activated PKA that reaches CREB in the nucleus, for instance (cf. Backsai, B.J. et al., *Science*, 260: 222-226 (1993); Kaang, B.K., et al., *Neuron*, 10: 427-435 (1993); Frank, D.A. and M.E. Greenberg, *Cell*, 79: 5-8 (1994)) -- is the rate-limiting step of LTM formation. Taken together, results from these experiments support the notion that the opposing functions of CREB activators and repressors act as a "molecular switch" (cf. Foulkes, N.S. et al., *Nature*, 355: 60-64 (1992)) to determine the parameters of extended training (number of training sessions and rest interval between them) required to form maximum LTM.

To date, seven different dCREB2 RNA isoforms have been identified, and more are hypothesized to exist. Each may be regulated differentially at transcriptional (Meyer, T.E., et al., *Endocrinology*, 132: 770-780 (1993)) and/or translation levels before or during LTM formation. In addition, different combinations of CREB isoforms may exist in different (neuronal) cell types. Consequently, many different combinations of activator and repressor molecules are possible. From this perspective, the notions that all activators and repressors are induced during a training session or that all repressors inactivate faster than activators (see above) need not be true. Instead, the model requires only that ΔC (the net function of activators and repressors) is less than or equal to zero immediately after training and the increases with time (rest interval).

Theoretically, particular combinations of activator and repressor molecules in the relevant neuron(s) should

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determine the rest interval and/or number of training sessions necessary to produce maximum LTM for any particular task or species. Thus, the molecular identification and biochemical characterization of each CREB activator and repressor isoform used during LTM formation in fruit flies is the next major step toward establishing the validity of our proposed model. Similar experiments in other species may establish its generality.

CREB certainly is not involved exclusively with LTM. The *dCREB2* gene, for instance, is expressed in all fruit fly cells and probably acts to regulate several cellular events (Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)).

So, what defines the specificity of its effects on LTM? Specificity most likely resides with the neuronal circuitry involved with a particular learning task. For olfactory learning in fruit flies, for instance, CREB probably is modulated via the cAMP second messenger pathway. Genetic disruptions of other components of this pathway are known to affect olfactory learning and memory (Livingstone, M.S., et al., *Cell*, 37: 205-215 (1984); Drain, P. et al., *Neuron*, 6: 71-82 (1991); Levin, L.R., et al., *Cell*, 68: 479-489 (1992); Skoulakis, E.M., et al., *Neuron* 11: 197-208 (1993); Qiu, Y. and R.L. Davis, *Genes Develop.* 7: 1447-1458 (1993)). Presumably, the stimuli used during conditioning (training) stimulate the underlying neuronal circuits. The cAMP pathway is activated in (some) neurons participating in the circuit, and CREB-dependent regulation of gene expression ensues in the "memory cells". This neurobiological perspective potentially will be established in *Drosophila* by identifying the neurons in which LTM-specific CREB function resides. Experiments using a neuronal co-culture system in *Aplysia* already have contributed significantly to this issue (Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994) and references therein).

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The involvement of CREB in memory, or in the structural changes of neurons which underlie memory in vivo, also has been implicated in mollusks (Dash, P.K., *Nature*, 345: 718-721 (1990); Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994)) and in mice (Bourtchuladze, R., et al., *Cell*, 79: 59-68 (1994)). Ample evidence also exists for the involvement of the cAMP second messenger pathway in associative learning in *Aplysia* (Kandel, E.R., et al., *In Synaptic Function*, Edelman, G.M., et al. (Eds.), John Wiley and Sons, New York (1987); Byrne, J.H., et al., *In Advances in Second Messenger and Phosphoprotein Research*, Shenolikar, S. and A.C. Nairn (Eds.), Raven Press, New York, pp. 47-107 (1993)) and in rat hippocampal long-term potentiation (LTP), a cellular model of associative learning in vertebrates (Frey, U., et al., *Science*, 260: 1661-1664 (1993); Huang, Y.Y. and E.R. Kandel, *In Learning and Memory*, vol. 1, pp.74-82, Cold Spring Harbor Press, Cold Spring Harbor, NY (1994)). Finally, cellular and biochemical experiments have suggested that CREB function may be modulated by other second messenger pathways (Dash, P.K., et al., *Proc. Natl. Acad. Sci. USA* 88: 5061-5065 (1991); Ginty, D.D. et al., *Science*, 260: 238-241 (1993); deGroot, R.P. and P. Sassone-Corsi, *Mol. Endocrinol.*, 7: 145-153 (1993)). These observation suggest that CREB might act as a molecular switch for LTM in many species and tasks.

Finally, why might the formation of LTM require a molecular switch? Many associative events occur only once in an animal's lifetime. Forming long-term memories of such events would be unnecessary and if not counterproductive. Instead, discrete events experienced repeatedly are worth remembering. In essence, a recurring event comprises a relevant signal above the noise of one-time events. Teleologically, then, the molecular switch may act as an information filter to ensure that only discrete but

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recurring events are remembered. Such a mechanism would serve efficiently to tailor an individual's behavioral repertoire to its unique environment.

The present invention also relates to isolated DNA
5 having sequences which encode (1) a cyclic 3',5'-adenosine monophosphate (cAMP) responsive transcriptional activator, or a functional fragment thereof, or (2) an antagonist of a cAMP responsive transcriptional activator, or a functional
10 fragment thereof, or (3) both an activator and an antagonist, or functional fragments thereof of both.

The invention relates to isolated DNA having sequences which encode *Drosophila* dCREB2 isoforms, or functional analogues of a dCREB2 isoform. As referred to herein, a functional analogue of a dCREB2 isoform comprises at least
15 one function characteristic of a *Drosophila* dCREB2 isoform, such as a cAMP-responsive transcriptional activator function and/or an antagonistic repressor of the cAMP activator function. These functions (i.e., the capacity to mediate PKA-responsive transcription) may be detected by
20 standard assays (e.g., assays which monitor for CREB-dependent activation). For example, assays in F9 cells have been used extensively to study CREB-dependent activation because their endogenous cAMP-responsive system is inactive; (Gonzalez, G.A. et al., *Nature*, 337: 749-752
25 (1989); Masson, N. et al., *Mol. Cell Biol.*, 12: 1096-1106 (1992); Masson, N. et al., *Nucleic Acids Res.*, 21: 1163-1169 (1993)).

The invention further relates to isolated DNA having sequences which encode a *Drosophila* dCREB2 gene or a
30 functional fragment thereof. Isolated DNA meeting these criteria comprise nucleic acids having sequences identical to sequences of naturally occurring *Drosophila* dCREB2 and portions thereof, or variants of the naturally occurring sequences. Such variants include mutants differing by the

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addition, deletion or substitution of one or more nucleic acids.

The invention relates to isolated DNA that are characterized by (1) their ability to hybridize to a
5 nucleic acid having the DNA sequence in Figure 1A (SEQ ID NO.: 1) or its complement, or (2) by their ability to encode a polypeptide of the amino acid sequence in Figure 1A (SEQ ID NO.: 2) or functional equivalents thereof (i.e., a polypeptide which functions as a cAMP responsive
10 transcriptional activator), or (3) by both characteristics. Isolated nucleic acids meeting these criteria comprise nucleic acids having sequences homologous to sequences of mammalian CREB, CREM and ATF-1 gene products. Isolated nucleic acids meeting these criteria also comprise nucleic
15 acids having sequences identical to sequences of naturally occurring Δ CREB2 or portions thereof, or variants of the naturally occurring sequences. Such variants include mutants differing by the addition, deletion or substitution of one or more residues, modified nucleic acids in which
20 one or more residues is modified (e.g., DNA or RNA analogs), and mutants comprising one or more modified residues.

Such nucleic acids can be detected and isolated under high stringency conditions or moderate stringency
25 conditions, for example. "High stringency conditions" and "moderate stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 (see particularly 2.10.8-11) and pages 6.3.1-6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. et al., eds,
30 Vol. 1, Suppl. 26, 1991), the teachings of which are incorporated herein by reference. Factors such as probe length, base composition, percent mismatch between the hybridizing sequences, temperature and ionic strength influence the stability of nucleic acid hybrids. Thus,
35 high or moderate stringency conditions can be determined

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empirically, depending in part upon the characteristics of the known DNA to which other unknown nucleic acids are being compared for homology.

Isolated nucleic acids that are characterized by their ability to hybridize to a nucleic acid having the sequence in Figure 1A or its complement (e.g., under high or moderate stringency conditions) may further encode a protein or polypeptide which functions as a cAMP responsive transcriptional activator.

The present invention also relates to isolated DNA having sequences which encode an enhancer-specific activator, or a functional fragment thereof.

The invention further relates to isolated DNA having sequences which encode a *Drosophila* dCREB1 gene or a functional fragment thereof. Isolated DNA meeting these criteria comprise nucleic acids having sequences identical to sequences of naturally occurring *Drosophila* dCREB1 and portions thereof, or variants of the naturally occurring sequences. Such variants include mutants differing by the addition, deletion or substitution of one or more nucleic acids.

The invention further relates to isolated DNA that are characterized by (1) their ability to hybridize to a nucleic acid having the DNA sequence in Figure 5 (SEQ ID NO.: 7) or its complement, or (2) by their ability to encode a polypeptide of the amino acid sequence in Figure 5 (SEQ ID NO.: 8), or by both characteristics. Isolated DNA meeting these criteria also comprise nucleic acids having sequences identical to sequences of naturally occurring dCREB1 or portions thereof, or variants of the naturally occurring sequences. Such variants include mutants differing by the addition, deletion or substitution of one or more residues, modified nucleic acids in which one or more residues is modified (e.g., DNA or RNA analogs), and mutants comprising one or more modified residues.

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Such nucleic acids can be detected and isolated under high stringency conditions or moderate stringency conditions as described above, for example.

Fragments of the isolated DNA which code for polypeptides having a certain function can be identified and isolated by, for example, the method of Jasin, M., et al., U.S. Patent No. 4,952,501.

Nitric Oxide in Invertebrates: *Drosophila* dNOS Gene Codes for a Ca^{2+} /Calmodulin-Dependent Nitric Oxide Synthase

10 Nitric oxide (NO) is a gaseous mediator of a wide variety of biological processes in mammalian organisms. Applicants have cloned the *Drosophila* gene, dNOS, coding for a Ca^{2+} /calmodulin-dependent nitric oxide synthase (NOS). Presence of a functional NOS gene in *Drosophila*
15 provides conclusive evidence that invertebrates synthesize NO and presumably use it as a messenger molecule. Furthermore, conservation of an alternative RNA splicing pattern between dNOS and vertebrate neuronal NOS, suggests broader functional homology in biochemistry and/or
20 regulation of NOS.

NO is synthesized by nitric oxide synthases (NOSs) during conversion of L-arginine to L-citrulline (Knowels, R.G., et al., *Biochem. J.*, 298: 249 (1994); Nathan, C., et al., *J. Biol. Chem.*, 269: 13725 (1994); Marletta, M.A., *J. Biol. Chem.*, 268: 12231 (1993)). Biochemical
25 characterization of NOSs has distinguished two general classes: (i) constitutive, dependent on exogenous Ca^{2+} and calmodulin and (ii) inducible, independent of exogenous Ca^{2+} and calmodulin. Analyses of cDNA clones have
30 identified at least three distinct NOS genes in mammals (Bredt, D.S., et al., *Nature*, 351: 714-718 (1991); Lamas, S., et al., *Proc. Natl. Acad. Sci. USA*, 89: 6348-6352 (1992); Lyons, C.R., et al., *J. Biol. Chem.*, 267: 6370 (1992); Lowenstein, C.J., et al., *Proc. Natl. Acad. Sci. USA*, 89:

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6711 (1992); Sessa, W.C., et al., *J.Biol.Chem.*, 267: 15274 (1992); Geller, D.A., et al., *Proc. Natl. Acad. Sci. USA*, 90: 3491 (1993); Xie, Q. et al., *Science*, 256: 225-228 (1992)) neuronal, endothelial and macrophage, the former
5 two of which are constitutive and the latter of which is inducible. The nomenclature for these different isoforms used here is historical, as it is clear now that one or more isoforms can be present in the same tissues (Dinerman, J.L., et al., *Proc. Natl. Acad. Sci. USA*, 91: 4214-4218
10 (1994)).

As a diffusible free-radical gas, NO is a multifunctional messenger affecting many aspects of mammalian physiology [for reviews, see Dawson, T.M., et al., *Ann. Neurol.* 32: 297 (1992); Nathan, C., *FASEB J.* 6: 3051 (1992); Moncada, S., et al., *N. Eng. J. Med.*, 329: 2002-2012 (1993); Michel, T., et al., *Amer. J. Cardiol.* 72: 33C (1993); Schuman, E.M., et al., *Annu. Rev. Neurosci.* 17: 153-183 (1994)]. NO originally was identified as an
20 endothelium-derived relaxing factor responsible for regulation of vascular tone (Palmer, R.M.J., *Nature* 327: 524 (1987); Palmer, R.M.J., et al., *Nature* 333: 664 (1988); Ignarro, L.J., et al., *Proc. Natl. Acad. Sci. USA*, 84: 9265 (1987)) and as a factor involved with macrophage-mediated cytotoxicity (Marletta, M.A., et al., *Biochemistry* 21: 8706
25 (1988); Hibbs, J.B., et al., *Biochem. Biophys. Res. Comm.* 157: 87 (1989); Steuhr, D.J., et al., *J. Exp. Med.*, 169: 1543 (1989)). Since NO has been implicated in several physiological processes including inhibition of platelet aggregation, promotion of inflammation, inhibition of
30 lymphocyte proliferation and regulation of microcirculation in kidney (Radomski, M., et al., *Proc. Natl. Acad. Sci. USA* 87: 5193 (1990); Albina, J.E., *J. Immunol.* 147: 144 (1991); Katz, R., *Am. J. Physiol.* 261: F360 (1992); Ialenti, A., et al., *Eur. J. Pharmacol.* 211: 177 (1992)). More recently,
35 NO also has been shown to play a role in cell-cell

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interactions in mammalian central and peripheral nervous systems -- in regulating neurotransmitter release, modulation of NMDA receptor-channel functions, neurotoxicity, nonadrenergic noncholinergic intestinal relaxation (Uemura, Y., et al., Ann. Neurol. 27: 620-625 (1990)) and activity-dependent regulation of neuronal gene expression (Uemura, Y., et al., Ann. Neurol. 27: 620 (1990); Dawson, V.L., et al., Proc. Natl. Acad. Sci. USA 88: 6368 (1991); Lei, S.Z., et al., Neuron 8: 1087 (1992); Prast, H., et al., Eur. J. Pharmacol. 216: 139 (1992); Peunova, N., Nature 364: 450 (1993)). Recent reports of NO function in synaptogenesis and in apoptosis during development of the rat CNS (Bredt, D.S., Neuron 13: 301 (1994); Roskams, A.J., Neuron 13: 289 (1994)) suggest that NO regulates activity-dependent mechanism(s) underlying the organization of fine-structure in the cortex (Edelman, G.M., et al., Proc. Natl. Acad. Sci. USA 89: 11651-11652 (1992)). NO also appears to be involved with long-term potentiation in hippocampus and long-term depression in cerebellum, two forms of synaptic plasticity that may underlie behavioral plasticity (Bohme, G.A., Eur. J. Pharmacol. 199: 379 (1991); Schuman, E.M., Science 254: 1503 (1991); O'Dell, T.J., et al., Proc. Natl. Acad. Sci. USA 88: 11285 (1991); Shibuki, K., Nature 349: 326 (1991); Haley, J.E., et al., Neuron 8: 211 (1992); Zhuo, M., Science 260: 1946 (1993); Zhuo, M., et al., NeuroReport 5: 1033 (1994)). Consistent with these cellular studies, inhibition of NOS activity has been shown to disrupt learning and memory (Chapman, P.F., et al., NeuroReport 3: 567 (1992); Holscher, C., Neurosci. Lett. 145: 165 (1992); Bohme, G.A., et al., Proc. Natl. Acad. Sci. USA 90: 9191 (1993); Rickard, N.S., Behav. Neurosci. 108: 640-644 (1994)).

Many of the above conclusions are based on pharmacological studies using inhibitors of nitric oxide

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synthases or donors of NO. Interpretations of such studies usually are limited because the drugs interact with more than one target and they cannot be delivered to specific sites. A molecular genetic approach can overcome these problems, however, by disrupting a specific gene, the product of which may be one of the drug's targets. Recently, such an approach has been attempted in mice via generation of a knock-out mutation of the neuronal NOS (nNOS) (Huang, P.L., et al., Cell 75: 1273-1286 (1993)).

10 While nNOS mutants appeared fully viable and fertile, minor defects in stomach morphology and hippocampal long-term potentiation were detected (Huang, P.L., et al., Cell 75: 1273-1286 (1993); O'Dell, T.J., et al., Science 265: 542-546 (1994)). Moreover, some NOS enzymatic activity still

15 was present in certain regions of the brain, suggesting a role for other NOS genes in the CNS. While yielding some relevant information about one specific component of NO function, this nNOS disruption existed throughout development. Consequently, functional defects of NOS

20 disruption in adults could not be resolved adequately from structural defects arising during development. Genetic tools exist in *Drosophila*, in contrast, to limit disruptions of gene functions temporally or spatially.

To identify candidate *Drosophila* NOS homologs, a

25 fragment of the rat neuronal NOS cDNA (Bredt, D.S., et al., Nature 351: 714-718 (1991)) was hybridized at low stringency to a phage library of the *Drosophila* genome as described in Example 11. The rat cDNA fragment encoded the binding domains of FAD and NADPH (amino acids 979 - 1408 of

30 SEQ ID NO.: 11), which are cofactors required for NOS activity, and therefore were expected to be conserved in fruit flies. Several *Drosophila* genomic clones were identified with the rat probe and classified into eight contigs. Sequence analysis of three restriction fragments

35 from these genomic clones revealed one (2.4R) with high

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homology to mammalian NOSS. The deduced amino acid sequence of the ORF encoded within the 2.4R fragment indicated 40% identity to the rat neuronal NOS and binding sites for FAD and NADPH.

5 The 2.4R DNA fragment then was used to probe a *Drosophila* adult head cDNA library as described in Example 11, and eight clones were isolated. Restriction analysis indicated that all contained identical inserts and thus, defined a predominant transcript expressed by this
10 *Drosophila* gene. One clone (c5.3) was sequenced in both directions. The 4491 bp cDNA contained one long ORF of 4350 bp. The methionine initiating this ORF was preceded by ACAAG which is a good match to the translation start consensus (A/CAAA/C) for *Drosophila* genes (Cavener, D.R.,
15 Nucleic Acids Res 15: 1353-1361 (1987)). Conceptual translation of this ORF yielded a protein of 1350 amino acids with a molecular weight of 151,842 Da.

Comparison of the amino acid sequence of this deduced *Drosophila* protein (DNOS) (SEQ ID NO.: 9) to sequences of
20 mammalian NOSS revealed that DNOS is 43% identical to neuronal NOS (SEQ ID NO.: 11), 40% identical to endothelial NOS (SEQ ID NO.: 10) and 39% identical to macrophage NOS (SEQ ID NO.: 12). It also revealed similar structural motifs in DNOS (Figure 16A-16C). The C-terminal half of
25 the DNOS protein contains regions of high homology corresponding to the presumptive FMN-, FAD- and NADPH-binding sites. Amino acids thought to be important for making contacts with FAD and NADPH in mammalian NOSS (Bredt, D.S., et al., Nature 351: 714-718 (1991); Lamas,
30 S., et al., Proc. Natl. Acad. Sci. USA 89: 6348-6352 (1992); Lyons, C.R., et al., J. Biol. Chem. 267: 6370 (1992); Lowenstein, C.J., et al., Proc. Natl. Acad. Sci. USA 89: 6711 (1992); Sessa, W.C., et al., J. Biol. Chem. 267: 15274 (1992); Geller, D.A., et al., Proc. Natl. Acad. Sci. USA
35 90: 3491 (1993); Xie, Q. et al., Science 256: 225-228

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(1992)) are conserved in DNOS. The middle section of DNOS, between residues 215 and 746 of SEQ ID NO.: 9, showed the highest similarity to mammalian NOSs: it is 61% identical to the neuronal isoform and 53% identical to endothelial and macrophage isoforms. Sequences corresponding to the proposed heme- and calmodulin-binding sites in mammalian enzymes are well-conserved in DNOS. The region located between residues 643-671 of SEQ ID NO.: 9 has the characteristics of a calmodulin-binding domain (basic, amphiphilic α -helix) (O'Neil, K.T., et al., Trends Biochem. Sci. **15**: 59-64 (1990)). The amino acid sequence between these two sites is very well conserved among all four NOS proteins, suggesting the location of functionally important domains such as the arginine-binding site (Lamas, S., et al., Proc. Natl. Acad. Sci. USA **89**: 6348-6352 (1992)), tetrahydrobiopterine cofactor binding site or a dimerization domain. DNOS also has a PKA consensus site (Pearson, R.B., Meth. Enzymol. **200**: 62-81 (1991)) (at Ser-287 of SEQ ID NO.: 9) in a position similar to neuronal and endothelial NOSs.

The 214 amino acid N-terminal domain of DNOS shows no obvious homology to its equivalent portion of neuronal NOS or to the much shorter N-terminal domains of endothelial and macrophage NOSs. This region of DNOS contains an almost uninterrupted homopolymeric stretch of 24 glutamine residues. Such glutamine-rich domains, found in many *Drosophila* and vertebrate proteins, have been implicated in protein-protein interactions regulating the activation of transcription (Franks, R.G., Mech. Dev. **45**: 269 (1994); Gerber, H.-P., et al., Science **263**: 808 (1994); Regulski, M., et al., EMBO J. **6**: 767 (1987)). Thus, this domain of DNOS could be involved with protein-protein interactions necessary for localization and/or regulation of DNOS activity.

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The above sequence comparisons suggest that a *Drosophila* structural homolog of a vertebrate NOS gene was identified. The order of the putative functional domains in the DNOS protein is identical to that of mammalian enzymes (Figure 15B). Structural predictions based on several protein algorithms also indicate that general aspects of DNOS protein secondary structure (hydrophobicity plot, distribution of α -helices and β -strands) from the putative heme-binding domain to the C-terminus are similar to those of mammalian NOSs. DNOS also does not contain a transmembrane domain, as is the case for vertebrate NOSs. In addition to these general characteristics, several aspects of DNOS structure actually render it most like neuronal NOS: (i) the overall sequence similarity, (ii) the similarity of the putative calmodulin-binding site (55% identical to the neuronal NOS vs. 45% identical to endothelial NOS or vs. 27% identical to macrophage NOS) and (iii) the large N-terminal domain. Neuronal NOS and DNOS also do not contain sites for N-terminal myristoylation, which is the case for endothelial NOS (Lamas, S., et al., Proc. Natl. Acad. Sci. USA 89: 6348-6352 (1992)), nor do they have a deletion in the middle of the protein, which is the case for macrophage NOS (Xie, Q. et al., Science 256: 225-228 (1992)).

To establish that Applicants putative DNOS protein had nitric oxide synthase activity, the *dNOS* cDNA was expressed in 293 human embryonic kidney cells as described in Example 12, which have been used routinely in studies of mammalian NOSs (Bredt, D.S., et al., Nature 351: 714-718 (1991)). Protein extracts prepared from *dNOS*-transfected 293 cells as described in Example 12, contained a 150 kD polypeptide, which was recognized by a polyclonal antibody raised against the N-terminal domain of DNOS (Figure 17A, lane 293 + *dNOS*). This immunoreactive polypeptide was of a size expected for DNOS and was absent from cells transfected

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with just the pCGN vector alone (Figure 17A, lane 293 + vector).

Extracts made from dNOS-transfected 293 cells showed significant NO synthase activity, as measured by the L-arginine to L-citrulline conversion assay as described in Example 12 (0.1276 ± 0.002 pmol/mg/min; Figure 17B, group B). [In a parallel experiment, the specific activity of rat neuronal NOS expressed from the same vector in 293 cells was 3.0 ± 0.02 pmol/mg/min, N=4]. DNOS activity was dependent on exogenous Ca^{2+} /calmodulin and on NADPH, two cofactors necessary for activity of constitutive mammalian NOSs (Iyengar, R., Proc. Natl. Acad. Sci. USA **84**: 6369-6373 (1987); Bredt, D.S., Proc. Natl. Acad. Sci. USA **87**: 682-685 (1990)). DNOS activity was reduced 90% by the Ca^{2+} chelator EGTA (Figure 17B, group C). Also, $500\mu\text{M}$ N-(6-aminohexyl)-1-naphthalene-sulfonamide (W5), a calmodulin antagonist which inhibits activity of neuronal NOS (Bredt, D.S., Proc. Natl. Acad. Sci. USA **87**: 682-685 (1990)), diminished DNOS activity to 18% (0.0222 ± 0.001 pmol/mg/min, N=2). In the absence of exogenous NADPH, DNOS (or nNOS) activity was reduced 20% (0.1061 ± 0.011 pmol/mg/min, N=4 for DNOS; 2.7935 ± 0.033 pmol/mg/min, N=2 for nNOS). DNOS activity also was blocked by inhibitors of mammalian NOSs (Rees, D.D., Br. J. Pharmacol., **101**: 746-752 (1990)). N^G -nitro-L-arginine methyl ester (L-NAME) reduced DNOS activity 84% (Figure 17B, group D), and $100\mu\text{M}$ N^G -monomethyl-L-arginine acetate produced a complete block (0.0001 ± 0.0002 pmol/mg/min, N=2). These enzymatic data demonstrate that DNOS is a Ca^{2+} /calmodulin-dependent nitric oxide synthase.

Northern blot analysis indicated a 5.0 kb dNOS transcript which was expressed predominantly in adult fly heads but not bodies (Figure 18A). More sensitive RT-PCR experiments as described in Example 13, however, detected dNOS message in poly(A)⁺ RNA from fly bodies. Neuronal NOS

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genes from mice and humans produce two alternatively spliced transcripts, the shorter one of which yields a protein containing a 105 amino acid in-frame deletion (residues 504-608 in mouse or rat neuronal NOS) (Ogura, T.,
5 Biochem. Biophys. Res. Commun. 193: 1014-1022 (1993)). RT-PCR amplification of *Drosophila* head mRNA produced two DNA fragments: the 444 bp fragment corresponded to vertebrate long form and the 129 bp fragment corresponded to vertebrate short form (Figure 18B). Conceptual translation
10 of the 129 bp sequence confirmed a splicing pattern identical to that for the nNOS gene (Figure 18C). Presence of the short NOS isoform in *Drosophila* strengthens the notion that it may play an important role in NOS biochemistry.

15 The discovery of a NOS homolog in *Drosophila* provides definitive proof that invertebrates produce NO and, as suggested by recent reports, most likely use it for intercellular signaling. These data also suggest that a NOS gene was present in an ancestor common to vertebrates
20 and arthropods, implying that NOS has existed for at least 600 million years. Thus, it is expected that NOS genes are prevalent throughout the animal kingdom.

Consistent with this view are existing histochemical data. NOS activity has been detected in several
25 invertebrate tissue extracts: in *Lyngbya polyphemus* Radomski, M.W., Philos. Trans. R. Soc. Lond. B. Biol. Sci., 334: 129-133 (1992)), in the locust brain (Elphick, M.R., et al., Brain Res. 619: 344-346 (1993)), in the salivary gland of *Rhodnius prolixus* (Ribeiro, J.M.C., et al., FEBS
30 Let. 330: 165-168 (1993) (34)) and in various tissues of *Lyngbya stagnalis* (Elofsson, R., et al., NeuroReport 4: 279-282 (1993)). Applications of NOS inhibitors or NO-generating substances have been shown to modulate the activity of buccal motoneurons in *Lyngbya stagnalis*
35 (Elofsson, R., et al., NeuroReport 4: 279-282 (1993)) and

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the oscillatory dynamics of olfactory neurons in procerebral lobe of *Limax maximus* (Gelperin, A., Nature 369: 61-63 (1994)). NADPH-diaphorase staining, a relatively specific indicator of NOS protein in fixed
5 vertebrate tissue samples (Dawson, T.M., et al., Proc. Natl. Acad. Sci. USA 88: 7797 (1991); Hope, B.T., et al., Proc. Natl. Acad. Sci. USA 88: 2811 (1991)), also has suggested the presence of NOS in *Drosophila* heads (Muller, U., Naturwissenschaft 80: 524-526 (1993)). The present
10 molecular cloning of *dNOS* considerably strengthens the validity of these observations.

Sophisticated genetic analyses of NOS function are available in *Drosophila*. Classical genetics will allow the creation of point mutations and deletions in *dNOS*,
15 resulting in full or partial loss of *dNOS* function. Such mutations will permit detailed studies of the role of NOS during development.

The invention further relates to isolated DNA that are characterized by their ability to encode a polypeptide
20 of the amino acid sequence in Figure 16A-16C (SEQ ID NO.: 9) or functional equivalents thereof (i.e., a polypeptide which synthesizes nitric oxide). Isolated DNA meeting this criteria comprise amino acids having sequences homologous to sequences of mammalian NOS gene products (i.e.,
25 neuronal, endothelial and macrophage NOSs). The DNA sequence represented in SEQ ID NO.: 25 is an example of such an isolated DNA. Isolated DNA meeting these criteria also comprise amino acids having sequences identical to sequences of naturally occurring *dNOS* or portions thereof,
30 or variants of the naturally occurring sequences. Such variants include mutants differing by the addition, deletion or substitution of one or more residues, modified nucleic acids in which one or more residues is modified (e.g., DNA or RNA analogs), and mutants comprising one or
35 more modified residues.

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Such nucleic acids can be detected and isolated under high stringency conditions or moderate stringency conditions, for example. "High stringency conditions" and "moderate stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 (see particularly 2.10.8-11) and pages 6.3.1-6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. et al., eds, Vol. 1, Suppl. 26, 1991), the teachings of which are incorporated herein by reference. Factors such as probe length, base composition, percent mismatch between the hybridizing sequences, temperature and ionic strength influence the stability of nucleic acid hybrids. Thus, high or moderate stringency conditions can be determined empirically, depending in part upon the characteristics of the known DNA to which other unknown nucleic acids are being compared for homology.

Isolated DNA that are characterized by their ability to encode a polypeptide of the amino acid sequence in Figure 16A-16C, encode a protein or polypeptide having at least one function of a *Drosophila* NOS, such as a catalytic activity (e.g., synthesis of nitric oxide) and/or binding function (e.g., putative heme, calmodulin, FMN, FAD and NADPH binding). The catalytic or binding function of a protein or polypeptide encoded by hybridizing nucleic acid may be detected by standard enzymatic assays for activity or binding (e.g., assays which monitor conversion of L-arginine to L-citrulline). Functions characteristic of dNOS may also be assessed by in vivo complementation activity or other suitable methods. Enzymatic assays, complementation tests, or other suitable methods can also be used in procedures for the identification and/or isolation of nucleic acids which encode a polypeptide having the amino acid sequence in Figure 16A-16C or functional equivalents thereof.

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The present invention will now be illustrated by the following examples, which are not intended to be limiting in any way.

EXAMPLES

5 The following materials and methods were used in the work described in Examples 1 and 2.

Expression Cloning of dCREB1 and dCREB2

Standard protocols for expression cloning by DNA-binding (Ausubel, F., Current Protocols in Molecular
10 Biology, John Wiley and Sons, New York, 1994; Singh, H. et al., Cell, 52: 415-423 (1988)) were followed except as noted. A double-stranded, 3xCRE oligonucleotide was synthesized and cloned between the XbaI and KpnI sites of pGEM7Zf+ (Promega). The sequence of one strand of the
15 oligonucleotide was 5' CGTCTAGATCTATGACTGAATA
TGACGTAATATGACGTAATGGTACCAGATCTGGCC 3' (SEQ ID NO.: 17), with the CRE sites underlined. The oligonucleotide was excised as a BglIII/HindIII fragment and labeled by filling-in the overhanging ends with Klenow fragment in the
20 presence of [α^{32} P]dGTP, [α^{32} P]dCTP and unlabeled dATP and dTTP (Ausubel, F., Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1994)). Just prior to use, the labeled fragment was pre-absorbed to blank
25 nitrocellulose filters to reduce background binding. All other steps were as described (Ausubel, F., Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1994)). After secondary and tertiary lifts, positive clones were subcloned into pKS+ (Stratagene) and sequences.

Gel Shift Analysis

30 Gel-mobility shift assays were performed as in Ausubel, F., Current Protocols in Molecular Biology, John

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Wiley and Sons, New York, 1994, with the following modifications. The 4% polyacrylamide gel (crosslinking ratio 80:1) was cast and run using 5x Tris-glycine buffer (Ausubel, F., Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1994)) supplemented with 3mM MgCl₂. The oligonucleotides used as the DNA probes were boiled and slowly cooled to room temperature at a concentration of 50 µg/ml in 0.1M NaCl. 50 ng of double-stranded probe was end-labeled using polynucleotide kinase in the presence of 100 µCi of [³²P]ATP. The double-stranded oligonucleotides were purified on a native polyacrylamide gel and used in a mobility shift assay at about 0.5 ng/reaction.

For dCREB2, the original dCREB2-b cDNA was subcloned and subjected to site-directed mutagenesis to introduce restriction sites immediately 5' and 3' of the open reading frame. This open reading frame was subcloned into the pET11A expression vector (Novagen) and used to induce expression of the protein in bacteria. The cells containing this vector were grown at 30°C to an approximate density of 2x10⁸/ml and heat-induced at 37°C for 2 hours. The cells were collected by centrifugation and lysed according to Buratowski, S. et al., Proc. Natl. Acad. Sci., USA, 88: 7509-7513 (1991). The crude extract was clarified by centrifugation and loaded onto a DEAE column previously equilibrated with 50 mM TrisHCl, pH 8.0, 10% sucrose, 100 mM KCl. Step elutions with increasing amounts of KCl in the same buffer were used to elute the dCREB2-b protein, which was assayed using the gel mobility-shift assay. The peak fraction was dialyzed against the loading buffer and used in the binding experiment. The specific competitor that was used was the wild-type CRE oligonucleotide. The sequence of one strand of the double-stranded oligonucleotides used in the gel shift analysis are listed.

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For the first two oligonucleotides, wild-type and mutant CREs are underlined.

Wild-type 3xCRE (SEQ ID NO.: 18):

5' AAATGACGTAACGGAAATGACGTAACGGAAATGACGTAACG 3';

5 Mutant 3xmCRE (SEQ ID NO.: 19):

5' AAATGAATTAACGGAAATGAATTAACGGAAATGAATTAACGG 3';

Nonspecific competitor #1 (SEQ ID NO.: 20):

5' TGCACGGGTTTTTCGACGTTCACTGGTAGTGTCTGATGAGGCCGAAAGGCCGAAA
CGCGATGCCCATTAACCACCACGCTCAG 3';

10 Nonspecific competitor #2 (SEQ ID NO.: 21):

5' TCGACCCACAGTTTTCGGGTTTTTCGAGCAAGTCTGCTAGTGTCTGATGAGGCCG
AAAGGCCGAAACGCGAAGCCGTATTGCACCACGCTCATCGAGAAGGC 3';

Nonspecific competitor #3 (SEQ ID NO.: 22):

5' CTAGAGCTTGCAAGCATGCTTGCAAGCAAGCATGCTTGCAAGCATGCTTG
15 CAAGC 3';

Nonspecific competitor #4 (SEQ ID NO.: 23):

5' CTCTAGAGCGTACGCAAGCGTACGCAAGCGTACG 3'

For dCREB1, heat-induced bacterial extracts (Ausubel, F., Current Protocols in Molecular Biology, John Wiley and
20 Sons, New York, 1994) were made from the original phage
clone integrated by lysogeny. Extract from a bacteria
lysogenized with another plaque (which did not bind to CRE
sites) from the screen was used as a negative control.
Competition experiments were done using a 4-100 fold molar
25 excess (relative to the probe) of unlabeled, wild-type CRE
oligonucleotides or unlabeled, mutant CRE oligonucleotides.

Northern Blots

Total head and body RNA was isolated from flies
according to the protocol of Drain, P. et al., Neuron,
30 6:71-82 (1991). Total RNA from all other developmental
stages was a gift from Eric Schaeffer. All RNA samples
were selected twice on oligo-dT columns (5 Prime-3 Prime)
to isolate poly A+ RNA. Two µg of poly A+ RNA was
fractionated on 1.2% formaldehyde-formamide agarose gels,

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transferred to nitrocellulose and probed using an uniformly labeled, strand-specific, antisense RNA (aRNA) probe. The template for the synthesis of aRNA was one of the partial cDNA clones isolated from the library screen (pJY199).

- 5 This cDNA contained the carboxyl-terminal 86 amino acids of the dCREB2-b protein and about 585 bp of 3' untranslated mRNA. All Northern blots were washed at high stringency (0.1% SDS, 0.1xSSC, 65°C).

In situ Hybridization To Tissue Sections

- 10 Frozen frontal sections were cut and processed under RNase-free conditions, essentially as described in Nighorn, A. et al., Neuron, 6:455-467 (1991), with modifications for riboprobes as noted here. Digoxigenin-labeled riboprobes were made from pJY199 using the Genius kit (Boehringer-Mannheim). One μ g of Xba-linearized template and T3 RNA
15 polymerase was used to make the antisense probe, while one μ g of EcoRI-linearized template together with T7 RNA polymerase was used for the control sense probe. Alkaline hydrolysis (30 minutes at 60°C) was used to reduce the
20 average probe size to about 200 bases. The hydrolyzed probe was diluted 1:250 in hybridization solution (Nighorn, A. et al., Neuron, 6:455-467 (1991)), boiled, quickly cooled on ice, added to the slides and hybridized at 42°C overnight. The slides were then treated with RNase A (20
25 μ g/ml RNase A in 0.5 M NaCl/10 mM Tris pH8 for 1 hour at 37°C) prior to two 50°C washes. Digoxigenin detection was as described.

Reverse Transcription Coupled With the Polymerase Chain Reaction (RT-PCR) Analysis of dCREB2 and Identification of 30 Alternatively Spliced Exons

The template for reverse transcription coupled with the polymerase chain reaction (RT-PCR) was total RNA or poly A+ RNA isolated from *Drosophila* heads as in Drain, P.

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et al., Neuron, 6: 71-82 (1991). Total RNA used was exhaustively digested with RNase-free DNase I (50 μ g of RNA digested with 50 units of DNase I for 60-90' at 37°C followed by phenol, phenol/chloroform extraction, and ethanol precipitation) prior to use. Results from separate experiments indicate that this DNase-treatment effectively eliminates the possibility of PCR products derived from any contaminating genomic DNA. Two rounds of selection using commercial oligo-dT columns (5 Prime-3 Prime) were used to isolate poly A+ RNA from total RNA. The template for an individual reaction was either 100-200 ng of total RNA, or 10-20 ng of poly A+ RNA.

The RT-PCR reactions were performed following the specifications of the supplier (Perkin-Elmer) with a "Hot Start" modification (Perkin-Elmer RT-PCR kit instructions). All components of the RT reaction, except the rTth enzyme, were assembled at 75°C, and the reaction was initiated by adding the enzyme and lowering the temperature to 70°C. At the end of 15 minutes, the preheated (to 75°C) PCR components (including trace amounts of [α^{32} P]dCTP) were added quickly, the reaction tubes were put into a pre-heated thermocycler, and the PCR amplification begun. Cycling parameters for reactions (100 μ l total volume) in a Perkin-Elmer 480 thermocycler were 94°C for 60 seconds, followed by 70°C for 90 seconds. For reactions (50 μ l) in an MJ Minicycler the parameters were 94°C for 45 seconds and 70°C for 90 seconds.

All primers used in these procedures were designed to have 26 nucleotides complementary to their target sequence. Some primers had additional nucleotides for restriction sites at their 5' ends to facilitate subsequent cloning of the products. Primers were designed to have about 50% GC content, with a G or C nucleotide at their 3' most end and with no G/C runs longer than 3. For RT-PCR reactions with a given pair of primers, the Mg^{+2} concentration was

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optimized by running a series of pilot reactions, at Mg^{+2} concentrations ranging from 0.6 mM to 3.0 mM. Reaction products were analyzed on denaturing urea-polyacrylamide gels by autoradiography. Any product that appeared larger
5 than the band predicted from the cDNA sequence was purified from a preparative native gel, re-amplified using the same primers, gel-purified, subcloned and sequenced.

To verify that a given RT-PCR product was truly derived from RNA, control reactions were run to show that
10 the appearance of the product was eliminated by RNase A treatment of the template RNA. Also, products generated from reactions using total RNA as the template were re-isolated from reactions using twice-selected polyA+RNA as template.

15 Plasmids

Expression constructs for transient transfection experiments in *Drosophila* were made in the expression vector pAct5CPPA (Han, K. et al., *Cell*, 56: 573-583 (1989)) or in pAcQ. pAcQ is a close derivative of pAct5CPPA in
20 which the XbaI site at the 5' end of the 2.5 kb actin promoter fragment was destroyed and additional sites were inserted in the polylinker. pAc-dCREB1 was made by subcloning a KpnI-SacI fragment containing the complete dCREB1 open reading frame (from a cDNA subcloned into pKS+) into pAct5CPPA. pAc-PKA was constructed by subcloning an
25 EcoRV fragment encoding the *Drosophila* PKA catalytic subunit (Foster, J.L. et al., *J. Biol. Chem.*, 263: 1676-1681 (1988)) from a modified pHSREM1 construct (Drain, P. et al., *Neuron*, 6: 71-82 (1991)) into pAct5CPPA. To make
30 the 3xCRE-lacZ reporter construct for *Drosophila* cell culture, the double-stranded, wild-type 3xCRE oligonucleotide used in the gel shift analysis was cloned into the KpnI-XbaI backbone of HZ50PL (Hiromi, Y. and W.J. Gehring, *Cell*, 50: 963-974 (1987)), a reporter construct

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made for enhancer testing which has cloning sites in front of a minimal *hsp70* promoter-lacZ fusion gene.

RSV-dCREB2-a was constructed in a long series of cloning steps. Essentially, the activator-encoding open reading frame was first reconstructed on the plasmid pKS+ by sequentially adding each of the three exons (exons 2, 4 and 6) into the original cDNA of dCREB2-b, which had been subcloned from phage DNA into pKS+. Site-directed mutagenesis was used to introduce unique restriction enzyme sites both 5' and 3' of the dCREB2-b open reading frame, and these sites facilitated the subcloning process and allowed removal of 5' and 3' untranslated sequences. Once the activator was assembled, the resulting open reading frame was sequenced to confirm the cloning steps and moved into a modified RSV vector which contained a polylinker located between the RSV promoter and the SV40 polyadenylation sequences (RSV-0). RSV-dCREB2-b was made by moving the original dCREB2-b cDNA (which had been subcloned into pKS+) into RSV-0.

Other constructs used in experiments were: pCaE (pMtC) (Mellon, P.L. et al., *Proc. Natl. Acad. Sci. USA*, 86: 4887-4891 (1989)), which contains the cDNA for mouse PKA catalytic subunit cloned under the mouse metallothionein 1 promoter; RSV- β gal (Edlund, T. et al., *Science*, 230: 912-916 (1985)), which expresses the lacZ gene under control of the Rous sarcoma long terminal repeat promoter (Gorman, C.M. et al., *Proc. Natl. Acad. Sci. USA*, 79: 6777-6781 (1982)). RSV-CREB (Gonzalez, G.A. et al., *Nature*, 337: 749-752 (1989)) is a CREB cDNA fragment containing the 341-amino acid open reading frame under the RSV LTR-promoter in RSV-SG, and the D(-71) CAT reporter (Montminy, M.R. et al., *Proc. Natl. Acad. Sci. USA*, 83: 6682-6686 (1986)) which is a fusion of a CRE-containing fragment of the rat somatostatin promoter and the bacterial CAT coding region.

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F9 Cell Culture and Transfection

Undifferentiated F9 cells were maintained and transfected using the calcium phosphate method as described in Darrow, A.L. et al., "Maintenance and Use of F9 Teratocarcinoma Cells" *In Meth. Enzymol.*, v. 190 (1990), except that chloroquine was added to 100 mM immediately before transfection and precipitates were washed off ten hours after transfection, at which time the dishes received fresh chloroquine-free medium. Amounts of DNA in transfections were made equivalent by adding RSV-0 where required. Cells were harvested 30 hours after transfection. Extracts were made by three cycles of freeze/thawing, with brief vortexing between cycles. Particulate matter was cleared from extracts by ten minutes of centrifugation in the cold. β -galactosidase assays were performed as described in Miller, J.H., *Experiments in Molecular Genetics*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1972. CAT assays were performed as described in Sheen, J.Y. and B. Seed, *Gene*, 67: 271-277 (1988) using aliquots of extract heat-treated at 65°C for ten minutes and centrifuged for ten minutes to remove debris. Results reported are from three experiments run on different days with at least three dishes per condition within each experiment. Error bars represent standard error of the mean, with error propagation taken into account (Grossman, M. and H.W. Norton, *J. Hered.*, 71: 295-297 (1980)).

Drosophila Cell Culture and Transient Transfection

Schneider L2 cells in Schneider's medium (Sigma) supplemented with 10% fetal bovine serum (FBS) or Kc167 cells in D-22 medium (Sigma) supplemented with 10% FBS, were transfected by the calcium phosphate method essentially as described in Krasnow, M.A. et al., *Cell*, 57: 1031-1043 (1989), with the following differences. Kc167 cells were plated at 2×10^6 cells/ml and chloroquine was

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added to a final concentration of 100 mM immediately prior to transfection. A total of 10 μ g of plasmid DNA per dish was used for L2 transfections and 25 μ g per dish for Kc167 transfections. DNA masses in transfections were made equivalent with pGEM7Zf+ where required. Precipitates were left undisturbed on L2 cells until harvest, but for Kc167 cells the original medium was replaced with fresh, chloroquine-free medium after twelve hours. Cells were harvested thirty-six to forty-eight hours after transfection. Extracts were made and enzymatic assays performed as described above for F9 cells. Results reported for transfections are averages of at least three experiments run on different days, with at least duplicate dishes for each condition within experiments. Error bars represent standard error of the mean, with error propagation taken into account (Grossman, M. and H.W. Norton, *J. Hered.*, 71: 295-297 (1980)).

β -galactosidase (β gal) and Chloramphenicol Acetyl Transferase (CAT) Assays

β -galactosidase assays were run and activity calculated as described in Miller, J.H., *Experiments in Molecular Genetics*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1972. CAT assays were performed essentially according to Sheen, J.Y. and B. Seed, *Gene*, 67: 271-277 (1988)) using supernatants from heat-treated aliquots of extracts (65°C for 10 minutes and then centrifuged for 10 minutes). Relative activity was calculated according to Sheen, J.Y. and B. Seed, *Gene*, 67: 271-277 (1988)).

PKA-Responsive Transcriptional Activation by dCREB2-a

F9 cells were transiently transfected with 10 μ g of D(-71) CAT plasmid as a CRE-directed reporter. 5 μ g of RSV- β gal reporter was included in each dish as a

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normalization control for transfection efficiency. Different groups received 8 μ g of dCREB2-a expression vector and 4 μ g of PKA expression vector, separately or in combination. Results are expressed as CAT/ β gal enzyme activity ratios, standardized to values obtained with PKA-transfected dishes.

Transcriptional Effect of dCREB2-b and a Mutant Variant On PKA-Responsive Activation by dCREB2-a

F9 cells were transiently cotransfected with 10 μ g of D(-71) CAT along with the indicated combinations of the following expression constructs: RSV-dCREB2-a (5 μ g); pMtC (2 μ g); RSV-dCREB2-b (5 μ g); and RSV-mLZ-dCREB2-b, which expresses a leucine-zipper mutant of dCREB2-b (5 μ g). The DNA mass for each dish was made up to 27 μ g with RSV-O. Other experimental conditions are as described above under "PKA-Responsive Transcriptional Activation by dCREB2-a".

Transcriptional Activation of a CRE Reporter Gene by dCREB1 in Drosophila Schneider L2 cell culture

The cells were transiently transfected with a dCREB1 expression construct (1 μ g), with or without a construct which expresses *Drosophila* PKA. 3xCRE- β gal reporter (1 μ g) and the normalization Ac-CAT reporter (1 μ g) were included in each dish. Expression vectors not present in particular dishes were replaced by pACQ.

Example 1 Isolation and Characterization of dCREB2

Two different genes were isolated in a DNA-binding expression screen of a *Drosophila* head cDNA library using a probe containing three CRE sites (3xCRE). Many clones were obtained for the dCREB2 gene, while only one clone was obtained for dCREB1. The dCREB2 clones had two alternatively-spliced open reading frames, dCREB2-b and dCREB2-c (see Figure 2). These differed only in the

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presence or absence of exon 4 and in their 5' and 3' untranslated regions. The inferred translation product of *dCREB2-b* showed very high sequence similarity to the amino acid sequences of the basic region/leucine zipper (bZIP) domains of mammalian CREB (SEQ ID NO.: 4), CREM (SEQ ID NO.: 5) and ATF-1 (SEQ ID NO.: 6) (see Figure 1B).

Chromosomal *in situ* hybridization using a *dCREB2* probe localized the gene to a diffuse band at 17A2 on the X chromosome, a region which contains several lethal complementation groups (Eberl, D.F. et al., *Genetics*, 30: 569-583 (1992)).

To determine the DNA binding properties of *dCREB2-b*, the DNA binding activity of *dCREB2-b* was assayed using a gel mobility-shift assay. Bacterial extracts expressing the *dCREB2-b* protein retarded the migration of a triplicated CRE probe (3xCRE). The protein had lower, but detectable, affinity for a mutated 3xCRE oligonucleotide. Competition experiments using unlabeled competitor oligonucleotides showed that the binding of *dCREB2-b* to 3xCRE was specific with higher affinity for CRE sites than to nonspecific DNA. Together with the conserved amino acid sequence, this functional similarity suggested that *dCREB2* was a CREB family member.

The expression pattern of *dCREB2* was determined by Northern blot analysis of poly A+RNA from various developmental stages. A complex pattern with at least 12 different transcript sizes was found. Two bands of approximately 0.8 and 3.5 kb were common to all of the stages. The adult head contained transcripts of at least six sizes (0.8, 1.2, 1.6, 1.9, 2.3 and 3.5 kb). *In situ* hybridization to RNA in *Drosophila* head tissue sections showed staining in all cells. In the brain, cell bodies but not neuropil were stained.

dCREB2 has alternatively-spliced forms. Initial transfection experiments showed that the *dCREB2-c* isoform

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was not a PKA-responsive transcriptional activator. This information, together with the complex developmental expression pattern and the known use of alternative splicing of the CREM gene to generate PKA-responsive
5 activators (Foulkes, N. and P. Sassone-Corsi, *Cell*, 68: 411-414 (1992); Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)) suggested that additional domains might be required to code for an activator.

Reverse transcription coupled with the polymerase
10 chain reaction (RT-PCR) was used to identify new exons. Comparison of the genomic DNA sequence with that of cDNAs indicated the general exon/intron organization and assisted in the search for additional exons. Sense and antisense primers spaced across the *dCREB2-b* cDNA were synthesized
15 and used pairwise in RT-PCR reactions primed with *Drosophila* head RNA. Reactions with primers in exons 5 and 7 (see Figure 2) generated two products, one with the predicted size (compared with the cDNA clones) and one that was larger. The larger fragment was cloned and its
20 sequence suggested the presence of exon 6 (see Figure 1A; SEQ ID NO.: 1). A primer within exon 6 was synthesized, end-labeled and used to screen a *Drosophila* head cDNA library. Two clones were isolated, sequenced and found to be identical. This splicing isoform, *dCREB2-d*, confirmed
25 the splice junctions and exon sequence inferred from the RT-PCR products.

Initial attempts to isolate exon 2 proved difficult. The genomic sequence that separated exons 1 and 3 (see Figure 2) was examined and one relatively extensive open
30 reading frame (ORF) was identified. Three antisense primers, only one of which lay inside this ORF, were synthesized based on the intron sequence. Three sets of RT-PCR reactions were run in parallel, each using one of the three antisense primers and a sense primer in exon 1.
35 Only the reaction that used the antisense primer in the ORF

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produced a PCR product. The sequence of this product matched a continuous stretch of nucleotides from the genomic sequence, extending 3' from exon 1 past the splice junction in the *dCREB2-b* cDNA to the location of the antisense primer in the ORF. This fragment suggested that exon 1 might be extended in some mRNAs by use of an alternative 5' splice site located 3' to the site used to make *dCREB2-b*. Based on the newly-identified exon sequences, a sense primer was made. This primer was used with an antisense primer in exon 3 to generate a new product whose sequence established the location of the new 5' splice site. The sequence added to exon 1 by alternative 5' splice site selection is denoted exon 2. The exon 2 sequence also showed that the same 3' splice site was used both for the original cDNA and for exon 2. To independently verify this alternative splicing pattern, RT-PCR was carried out with a primer that spanned the 3' splice junction of exon 2 and a primer in exon 1. The sequence of the product corroborated the splice junctions of exon 2 shown in Figure 1A (SEQ ID NO.: 1).

To determine if exons 2 and 6 could be spliced into the same molecule, an RT-PCR reaction was carried out with primers in exons 2 and 6. The reaction produced a product of the size predicted by coordinate splicing of these two exons and the identity of this product was confirmed by extensive restriction analysis.

dCREB2 is a *Drosophila* CREB/ATF gene. Figure 1A shows the DNA sequence (SEQ ID NO.: 1) and inferred amino acid sequence (SEQ ID NO.: 2) of *dCREB2-a*, the longest ORF that can result from the identified alternative splicing events. The indicated translation start site for this ORF is probably authentic because: i) stop codons occur upstream from this ATG in all reading frames in our *dCREB2* cDNAs (sequences not shown) ii) this ATG was selected by computer (Sheen, J.Y. and B. Seed, *Gene*, 67: 271-277 (1988)) as the

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best ribosome binding site in the DNA sequence that contains the ORF; and iii) use of the next ATG in the open reading frame 480 nucleotides downstream would not produce an inferred product that is a PKA-dependent activator (see below). This information does not exclude the possibility that internal translation initiation sites may be used in this transcript, as happens in the CREM gene's S-CREM isoform (Delmas, V. et al., *Proc. Natl. Acad. Sci. USA*, 89: 4226-4230 (1992)).

10 The *dCREB2-a* open reading frame predicts a protein of 361 amino acids with a carboxyl-terminal bZIP domain (SEQ ID NO.: 3) highly homologous to those of mammalian CREB (SEQ ID NO.: 4) and CREM (SEQ ID NO.: 5) (see Figure 1B). The inferred *dCREB2-a* product has a small region of amino acids containing consensus phosphorylation sites for PKA, calcium/calmodulin-dependent kinase II (CaM kinase II) and protein kinase C (PKC) at a position similar to that of the P-box in CREB, CREM and ATF-1. The amino-terminal third of the predicted *dCREB2-a* is rich in glutamines (including runs of four and five residues). Glutamine-rich activation domains occur in CREB, CREM, and other eukaryotic transcription factors, including some from *Drosophila* (Courey, A.J. and R. Tijan, "Mechanisms of Transcriptional Control as Revealed by Studies of the Human Transcription Factor Sp1" *In Transcriptional Regulation*, vol. 2, McKnight, S.L. and K.R. Yamamoto (eds.), Cold Spring Harbor Press, Cold Spring Harbor, NY, 1992; Mitchell, P.J. and R. Tijan, *Science*, 245: 371-378 (1989)).

30 A computerized amino acid sequence homology search with the predicted *dCREB2-a* protein sequence (SEQ ID NO.: 2) identifies CREB, CREM and ATF-1 gene products as the closest matches to *dCREB2-a*. The homology is particularly striking in the carboxyl-terminal bZIP domain where 49 of 54 amino acids are identical with their counterparts in mammalian CREB (Figure 1B). The homology

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is less striking, albeit substantial, in the activation domain. Lower conservation in this domain is also characteristic of the mammalian CREB and CREM genes (Masquillier, D. et al., *Cell Growth Differ.*, 4: 931-937 (1993)).

Figure 2 shows the exon organization of all of the dCREB2 alternative splice forms that we have detected, both as cDNAs and by RT-PCR. Splice products of dCREB2 fall into two broad categories. One class of transcripts (dCREB2-a, -b, -c, -d) employs alternative splicing of exons 2, 4 and 6 to produce isoforms whose protein products all have the bZIP domains attached to different versions of the activation domain. The second class of transcripts (dCREB2-q, -r, -s) all have splice sites which result in in-frame stop codons at various positions upstream of the bZIP domain. These all predict truncated activation domains without dimerization or DNA binding activity.

Two different dCREB2 isoforms, dCREB2-a and dCREB2-b, have opposite roles in PKA-responsive transcription. The capacity of isoforms of the dCREB2 gene to mediate PKA-responsive transcription was tested in F9 cells. These cells have been used extensively to study CREB-dependent activation because their endogenous cAMP-responsive transcription system is inactive (Gonzalez, G.A. et al., *Nature*, 337: 749-752 (1989); Masson, N. et al., *Mol. Cell Biol.*, 12: 1096-1106 (1992); Masson, N. et al., *Nucleic Acids Res.*, 21: 1163-1169 (1993)). Candidate cAMP-responsive transcription factors, synthesized from expression vectors, were transiently transfected with and without a construct expressing the PKA catalytic subunit. CREB-dependent changes in gene expression were measured using a cotransfected construct that has a CRE-containing promoter fused to a reporter gene.

The product of the dCREB2-a isoform is a PKA-dependent activator of transcription (Figure 3). Transfection of PKA

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or dCREB2-a alone gave only modest activation above baseline values. Cotransfection of dCREB2-a and PKA together, however, gave levels of activation 5.4-fold greater than the activation seen with PKA alone.

5 dCREB2-b did not act as a PKA-dependent transactivator. When transfected together with the reporter and PKA, it failed to stimulate reporter activity. Instead, it functioned as a direct antagonist of PKA-dependent activation by dCREB2-a (Figure 4). Cotransfection
10 of equimolar amounts of the dCREB2-a and dCREB2-b expression constructs, along with PKA and the reporter, resulted in a nearly complete block of PKA-dependent activation from the CRE-containing reporter.

The strong homology between the leucine zippers of
15 dCREB2 (SEQ ID NO.: 3), CREB (SEQ ID NO.: 4) and CREM (SEQ ID NO.: 5) (see Figure 1B) suggested that mutations which abolish CREB dimerization (Dwarki, V.J. et al., EMBO J., 9: 225-232 (1990)) should also affect dCREB2 dimerization. The mutant *Drosophila* molecule mLZ-dCREB2-b was made by
20 introducing two single-base changes that convert the middle two leucines of the leucine zipper to valines. An identical mutation in CREB abolishes homodimerization in vitro (Dwarki, V.J. et al., EMBO J., 9: 225-232 (1990)). Cotransfected mLZ-dCREB2-b failed to block PKA-dependent
25 activation by dCREB2-a (Figure 4).

Example 2 Isolation and Characterization of dCREB1

A single cDNA representing the dCREB1 gene was isolated in the same screen of a *Drosophila* lambda gt11 expression library that yielded the dCREB2 cDNAs. The
30 sequence of the dCREB1 cDNA contained a complete open reading frame specifying a 266 amino acid protein with a carboxyl-terminal leucine zipper four repeats long and an adjacent basic region (Figure 5; SEQ ID NO.: 7). The amino-terminal half of the inferred protein contains an

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acid-rich activation domain, with glutamate, aspartate and proline residues spaced throughout. *dCREB1* has consensus phosphorylation sites for CaM kinase II and PKC throughout its length, but has no predicted phosphoacceptor site for
5 PKA.

Gel shift analysis showed higher-affinity binding of the *dCREB1* protein to 3xCRE than to 3xmCRE. Transcriptional activation by *dCREB1* was assayed with transient cotransfection experiments using the *Drosophila*
10 L2 and Kc167 cell culture lines. In L2 cells, *dCREB1* activates transcription from CREs, but this effect is not enhanced by cotransfection of PKA (Figure 6). In Kc167 cells, *dCREB1* fails to activate reporter expression either alone or with cotransfected PKA expression constructs.

15 Genomic Southern blot analysis indicates that *dCREB1* is a single copy gene, and chromosomal *in situ* hybridization shows that it is located at 54A on the right arm of chromosome 2.

These results show that *dCREB1* is a non-PKA responsive
20 CREB family member from *Drosophila*.

The following materials and methods were used in the work described in Examples 3 and 4.

Isolating Transgenic Flies

EcoRI restriction sites were added (using PCR) just 5'
25 to the putative translation initiation site and just 3' to the translation termination site in the *dCREB2-b* cDNA. This fragment was sequenced and subcloned into CaSpeR hs43, a mini-white transformation vector which contains the *hsp70* promoter, in the orientation so that the *dCREB2-b* open
30 reading frame is regulated by the *hsp70* promoter. Germ-line transformation was accomplished using standard techniques (Spradling, A.C. and G.M. Rubin, *Science*, 218: 341-347 (1982); Rubin, G.M. and A. Spradling, *Science*, 218:

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348-353 (1982)). Two transgenic lines, 17-2 and *M11-1*, each with one independent P-element insertion were generated and characterized. They appeared normal in general appearance, fertility and viability. These
5 transgenic lines were outcrossed for at least five generations to *w*(CS-10) (Dura, J-M., et al., *J. Neurogenet.* 9: 1-14 (1993)), which itself had been outcrossed for ten generations to a wild-type (Can-S) stock. This extensive series of outcrossing is necessary to equilibrate the
10 genetic background to that of Canton-S. Flies homozygous for the 17-2 transgene were bred and used for all experiments.

The mutant blocker has been described previously (see Example 1). The mutations were substituted into an
15 otherwise wild-type blocker construct and germ-line transformants were made by injecting into *w(isoCJ1)* embryos. Flies homozygous for the A2-2 transgene insertion were bred and used for all experiments. *w(isoCJ1)* is a subline of *w(CS10)* (see above) carrying
20 isogenic X, 2nd and 3rd chromosomes and was constructed by Dr. C. Jones in our laboratory. Originally 40 such sublines were *w(CS10)* using standard chromosome balancer stocks. Olfactory acuity, shock reactivity, learning and three-hr memory after one-cycle training then were assayed
25 in each isogenic subline. As expected, a range of scores among the sublines was obtained. *w(isoCJ1)* yielded scores that were most like those of *w(CS10)* on each of these assays. By injecting DNA into the relatively homogeneous genetic background of *w(isoCJ1)*, outcrossing of the
30 resulting germ-line transformants to equilibrate heterogeneous) genetic backgrounds was not necessary.

Cycloheximide Feeding and Heat-Shock Regimen

For experiments on memory retention after one-cycle training and on retrograde amnesia, flies were fed 35 mM

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cycloheximide (+CMX; Sigma) in 4% sucrose (w/v) or 4% sucrose alone (-CXM) at 25°C. Groups of 100 flies were placed in feeding tubes (Falcon 2017) containing two 1.0 x 2.5 cm Whatmann 3MM filter paper strips that were soaked
5 with a total of 250 μ l of solution.

For experiments on one day retention after massed or spaced training, flies were fed 35 mM CXM and (w/v) 5% glucose dissolved in 3% ethanol. Groups of 100 flies were placed in feeding tubes (Falcon 2017) containing one 1.0 x
10 2.5 cm Whatmann 3MM filter paper strips that was soaked with a total of 126 μ l of solution.

For experiments on learning after one-cycle training, olfactory acuity, and shock reactivity, flies were fed a 5% glucose, 3% ethanol solution alone or 35 mM CXM in the
15 glucose/ethanol solution.

The feeding period was limited to 12-14 hrs prior to training, or to the 24-hr retention interval after training. Flies which were fed prior to training were transferred directly to the training apparatus after
20 feeding, subjected to massed or spaced training, then transferred to test tubes containing filter paper strips soaked with 5% glucose during the 24-hr interval. Flies which were fed after training were trained, then transferred immediately to test tubes containing filter
25 paper strips soaked with 5% glucose solution which was laced with 35 mM CXM. Flies remained in the test tubes for the duration of the 24-hr retention interval.

For heat-shock induction, flies were collected within two days of eclosion, placed in glass bottles in groups of
30 about 600, and incubated overnight at 25° C and 70% relative humidity. The next day, three hours before training, groups of approximately 100 flies were transferred to foam-stoppered glass shell vials containing a strip of filter paper to absorb excess moisture. The
35 vials then were submerged in a 37°C water bath until the

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bottom of the foam stopper (inside the vial) was below the surface of the water, thereby insuring that the flies could not escape heat-shock. The vial remained submerged for 30 min, after which the flies were transferred to a standard food vial for a 3-hr recovery period at 25° C and 70% relative humidity. Training began immediately after the recovery period.

Pavlovian Learning and Memory and Testing

Flies were trained with an automated version of the learning procedure of Tully, T. and W.G. Quinn, *J. Comp. Physiol.*, 157: 263-277 (1985). In brief, flies were trapped in a training chamber, the inside of which was covered with an electrifiable copper grid. Groups of about 100 flies were exposed sequentially to two odors [either octanol (OCT) or methylcyclohexanol (MCH)], which were carried through the training chamber in a current of air, for 60 seconds with 45 seconds rest intervals after each odor presentation. During exposure to the first odor, flies also were subjected to twelve 1.5-second pulses of 60 V DC with a 5-second interpulse interval. After training, flies were transferred to food vials for a particular retention interval. Conditioned odor-avoidance responses then were tested by transferring flies to the choice point of a T-maze, where they were exposed simultaneously to OCT and MCH carried in the distal ends of the T-maze arms and out the choice point on converging currents of air. Flies were allowed to distribute themselves in the T-maze arms for two minutes, after which they were trapped in their respective arms, anesthetized and counted. The "percent correct" then was calculated as the number of flies avoiding the shock-paired odor (they were in the opposite T-maze arm) divided by the total number of flies in both arms. (The number of flies left at the choice point, which usually was less than 5%, were not included in this calculation). Finally, a

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performance index (PI) was calculated by averaging the percent corrects of two reciprocal groups of flies -- one where OCT and shock were paired, the other where MCH and shock were paired -- and then by normalizing the average so that a PI=0 represented a 50:50 distribution in the T-maze and a PI=100 represented 100% avoidance of the shock-paired odor. For these studies, three different training protocols were used: 1. One-cycle training consisted of the training session just described. 2. Massed training consisted of 10 of these training cycles delivered one right after the other. 3. Spaced training consisted of 10 training cycles with a 15-min rest interval between each. One-cycle training was used to assay learning, while massed and spaced was used to assay consolidated memories.

15 Olfactory Acuity and Shock Reactivity

Odor avoidance responses to OCT or to MCH at two different concentrations -- one (10^0) usually used in conditioning experiments and a 100-fold (10^{-2}) dilution thereof -- were quantified in various groups of flies in the absence of heat shock and 3 hr or 24 hr after heat shock with the method of Boynton, S. and T. Tully, *Genetics*, 131: 655-672 (1992). Briefly, flies are placed in a T-maze and given a choice between an odor and air. The odors are naturally aversive, and flies usually choose air and avoid the T-maze arm containing the odor. For shock reactivity, flies are given a choice between an electrified grid in one T-maze arm, and an unconnected grid in the other. After the flies have distributed themselves, they are anesthetized, counted and a PI is calculated.

30 Statistical Analyses of Behavioral Data

Since each PI is an average of two percentages, the Central Limit Theorem predicts that they should be distributed normally (see Sokal, R.R. and F.J. Rohlf,

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Biometry, 2nd Edition, W.H. Freeman and Company, New York (1981)). This expectation was shown to be true by an empirical determination with data from Tully, T. and W.G. Quinn, *J. Comp. Physiol.*, 157: 263-277 (1985) and Tully, T. and D. Gold, *J. Neurogenet.*, 9: 55-71 (1993). Thus, untransformed (raw) data were analyzed parametrically with JMP2.1 statistical software (SAS Institute Inc., Cary NC). Since preliminary experiments preceded all of the experiments summarized herein, all pairwise comparisons were planned. To maintain an experimentwise error rate of $\alpha = 0.05$, the critical P values for these individual comparisons were adjusted accordingly (Sokal, R.R. and F.J. Rohlf, *Biometry*, 2nd Edition, W.H. Freeman and Company, New York (1981)) and are listed below for each experiment.

All experiments were designed in a balanced fashion with N=2 PIs per group collected per day; then replicated days were added to generate final Ns. In each experiment, the experimenter (M.D.) was blind to genotype.

A. One-day memory in wild-type flies fed CXM before or immediately after massed or spaced training (Figure 8): PIs from these four drug treatments (-CXM before, -CXM after, +CXM before and +CXM after) and two training procedures (massed and spaced) were subjected to a TWO-WAY ANOVA with DRUG ($F_{(3,56)} = 8.93$; $P < 0.001$) and TRAINING ($F_{(1,56)} = 18.10$, $P < 0.001$) as main effects and DRUG x TRAIN ($F_{(3,56)} = 4.68$, $P = 0.006$) as the interaction term. P values from subsequent planned comparisons are summarized in Figure 8. The six planned comparisons were judged significant if $P \leq 0.01$.

B. One-day memory after massed or spaced training in dCREB2-b transgenic flies (Figures 9A and 9B): In experiments with the 17-2 transgenic line, PIs from two strains (Can-S and 17-2) and four training-regimens

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(spaced-hs, spaced+hs, massed-hs and massed+hs) were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(1,40)} = 1.57$; $P = 0.22$) and TRAINing-regimen ($F_{(3,40)} = 25.81$, $P < 0.001$) as main effects and STRAIN x TRAIN ($F_{(3,40)} = 6.62$, $P = 0.001$) as the interaction term. A similar analysis was done with data from the M11-1 transgenic line, yielding STRAIN ($F_{(1,40)} = 2.81$; $P = 0.10$), TRAINing-regimen ($F_{(3,40)} = 11.97$, $P < 0.001$) and STRAIN x TRAIN ($F_{(3,40)} = 3.37$, $P = 0.03$) effects. P values from subsequent planned comparisons are summarized in Figures 9A and 9B. In each experiment, the seven planned comparisons were judged significant if $P \leq 0.01$.

C. Learning after one-cycle training in 17-2 transgenic flies (Figure 9C): PIs from two strains (Can-S and 17-2) and three heat-shock regimens [-hs, +hs (3 hr) and +hs (24 hr)] were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(1,30)} = 0.69$; $P = 0.41$) and HEAT-shock regimen ($F_{(2,30)} = 10.29$, $P < 0.001$) as main effects and STRAIN x HEAT ($F_{(2,30)} = 0.71$, $P = 0.50$) as the interaction term. P values from subsequent planned comparisons are summarized in Figure 9C. The three planned comparisons were judged significant if $P \leq 0.02$.

D. One-day memory after spaced training in A2-2 transgenic flies (Figure 10): PIs from these three strains [w(isoCJ1), 17-2 and A2-2] and two heat-shock regimens [-hs and +hs (3 hr)] were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(2,30)} = 9.43$, $P < 0.001$) and HEAT-shock regimen ($F_{(1,30)} = 9.84$, $P = 0.004$) as main effects and STRAIN x HEAT ($F_{(2,30)} = 5.71$, $P = 0.008$) as the interaction term. P values from subsequent comparisons are summarized in Figure 10. The six planned comparisons were judged significant if $P \leq 0.01$.

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E. Olfactory acuity in 17-2 flies (Table): PIs from these two strains (Can-S and 17-2), four different odor-levels (OCT- 10^0 , OCT- 10^{-2} , MCH- 10^0 and MCH- 10^{-2}) and three heat-shock regimens [-hs. +hs (3 hr) and +hs (24 hr)] were subjected to a THREE-WAY ANOVA with STRAIN ($F_{(1,184)} = 0.12$, $P = 0.73$), ODOR-level ($F_{(3,184)} = 126.77$, $P < 0.001$) and HEAT-shock regimen ($F_{(2,184)} = 3.55$, $P = 0.03$) as main effects, STRAIN x ODOR ($F_{(3,184)} = 1.23$, $P = 0.30$), STRAIN x HEAT ($F_{(2,184)} = 0.33$, $P = 0.72$) and ODOR x HEAT ($F_{(6,184)} = 3.14$, $P = 0.006$) as two-way interaction terms and STRAIN x ODOR x HEAT ($F_{(6,184)} = 0.48$, $P = 0.83$) as the three-way interaction term. P values from subsequent planned comparisons are summarized in the Table. The twelve planned comparisons were significant if $P \leq 0.005$.

F. Shock reactivity in 17-2 flies (Table): PIs from these two strains (Can-S and 17-2), two shock groups (60V and 20V) and three heat-shock regimens [-hs, +hs (3 hr) and +hs (24 hr)] were subjected to a THREE-WAY ANOVA with STRAIN ($F_{(1,84)} = 0.50$, $P = 0.48$), SHOCK ($F_{(1,84)} = 97.78$, $P < 0.001$) and HEAT-shock regimen ($F_{(2,84)} = 3.36$, $P = 0.04$) as main effects, STRAIN x SHOCK ($F_{(1,84)} = 1.12$, $P = 0.29$), STRAIN x HEAT ($F_{(2,84)} = 1.06$, $P = 0.35$) and SHOCK x HEAT ($F_{(2,84)} = 6.66$, $P = 0.002$) as two-way interaction terms and STRAIN x SHOCK x HEAT ($F_{(2,84)} = 1.75$, $P = 0.18$) as the three-way interaction term. P values from subsequent planned comparisons are summarized in the Table. The six planned comparisons were judged significant if $P \leq 0.01$.

G. Seven-day memory after spaced training in 17-2 flies (Figure 11): PIs from two strains (Can-S and 17-2) and two heat-shock regimens [-hs and +hs(3 hr)] were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(1,20)} = 6.09$; $P = 0.02$) and HEAT-shock regimen ($F_{(1,20)} = 16.30$, $P = 0.001$) as main effects and STRAIN x TRAIN ($F_{(1,20)} = 7.73$, $P = 0.01$) as

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the interaction term. P values from subsequent planned comparisons are summarized in Figure 11. The three planned comparisons were judged significant if $P \leq 0.02$.

H. One-day memory after spaced training in *rsh;17-2* double mutants (Figure 12): PIs from three strains (17-2, *rsh* and *rsh;17-2*) and two heat-shock regimens [-hs and +hs (3 hr)] were subjected to a TWO WAY ANOVA with STRAIN ($F_{(2,30)} = 32.05$; $P < 0.001$) and HEAT-shock regimen ($F_{(1,30)} = 59.68$, $P < 0.001$) as main effects and STRAIN x TRAIN ($F_{(2,30)} = 11.59$, $P < 0.001$) as the interaction term. P values from subsequent planned comparisons are summarized in Figure 12. The five planned comparisons were judged significant if $P \leq 0.01$.

I. Learning after one-cycle training in *rsh;17-2* mutants (see text): PIs from these two strains (Can-S and *rsh;17-2*) and two heat-shock regimens [-hs and +hs (3 hr)] were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(1,20)} = 86.85$, $P < 0.001$) and HEAT-shock regimen ($F_{(1,20)} = 0.02$, $P < 0.89$) as main effects and STRAIN x HEAT ($F_{(1,20)} = 0.86$, $P = 0.37$) as the interaction term. P values from subsequent planned comparisons are summarized in the Table. The two planned comparisons were significant if $P \leq 0.03$.

J. Olfactory acuity in *rsh;17-2* flies (Table): PIs from these two strains (Can-S and *rsh;17-2*), four different odor-levels (OCT- 10^0 , OCT- 10^{-2} , MCH- 10^0 and MCH- 10^{-2}) and two heat-shock regimens [-hs, and +hs (3 hr)] were subjected to a THREE-WAY ANOVA with STRAIN ($F_{(1,112)} = 0.02$, $P = 0.88$), ODOR-level ($F_{(3,112)} = 50.03$, $P < 0.001$) and HEAT-shock regimen ($F_{(1,112)} = 29.86$, $P < 0.001$) as main effects, STRAIN x ODOR ($F_{(3,112)} = 2.15$, $P = 0.10$), STRAIN x HEAT ($F_{(1,112)} = 0.34$, $P = 0.56$) and ODOR x HEAT ($F_{(3,112)} = 6.41$, $P = 0.001$) as two-way interaction terms and STRAIN x ODOR x HEAT

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($F_{(3,112)} = 1.12$, $P = 0.35$) as the three-way interaction term. P values from subsequent planned comparisons are summarized in the Table. The eight planned comparisons were judged significant if $P \leq 0.01$.

- 5 K. Shock reactivity in *rsh;17-2* flies (Table): PIs from these two strains (Can-S and *rsh;17-2*), two shock groups (60V and 20V) and two heat-shock regimens [-hs and +hs (3 hr)] were subjected to THREE-WAY ANOVA with STRAIN ($F_{(1,56)} = 0.51$, $P = 0.48$), SHOCK ($F_{(1,56)} = 88.14$, $P < 0.001$) and HEAT-shock regimen ($F_{(1,56)} = 0.08$, $P = 0.77$) as main effects, STRAIN x SHOCK ($F_{(1,56)} = 0.12$, $P = 0.73$, STRAIN x HEAT ($F_{(1,56)} = 0.03$, $P = 0.86$) and SHOCK x HEAT ($F_{(1,56)} = 0.39$, $P = 0.53$) as two-way interaction terms and STRAIN x SHOCK x HEAT ($F_{(1,84)} = 1.58$, $P = 0.21$) as the three-way interaction term. P values from subsequent planned comparisons are summarized in the Table. The four planned comparisons were judged significant if $P \leq 0.01$.

Northern Analysis

- For RNA collection, the heat-shock regimen was the same as for behavioral experiments. For any indicated time interval between heat-shock and collection, flies rested in food-containing vials at 25°C. Flies were collected and quickly frozen in liquid nitrogen. All Northern analyses used head RNA. The tube of frozen flies was repeatedly rapped sharply on a hard surface, causing the heads to fall off. The detached frozen heads were recovered by sieving on dry ice. Approximately 1000 heads were pooled for RNA preparation. Wild-type and transgenic flies for each individual time point always were processed in parallel. Flies that were not induced were handled in a similar manner to induced flies, except that the vials were not placed at 37°C. Total head RNA was isolated from each group of flies, and poly A+ RNA was isolated using oligo dT

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columns according to the instructions of the manufacturer (5'--->3' Inc.). The concentration of poly A+ mRNA was measured spectrophotometrically, and 0.5 mg of mRNA per lane was loaded and run on 1.2% formaldehyde-agarose gels.

5 Northern blots were prepared, probed and washed (0.1 x SSC at 65°C) as described (Ausubel, F., *Current Protocols in Molecular Biology*, John Wiley and Sons, New York, 1994). For detection of the transgene, an 843bp dCREB2-b cDNA fragment was subcloned into pKS+ and used to generate a

10 uniformly-labeled antisense riboprobe. This fragment codes for the carboxyl-terminal 86 amino acids of the dCREB2-b protein plus 3' untranslated mRNA.

Western Blot Analysis and Antiserum

Western blot analysis was performed using a rabbit

15 antiserum raised against a peptide corresponding to 16 amino acids in the basic region of the dCREB2-b cDNA with an additional COOH terminal Cys. The sequence of the peptide was: (SEQ ID NO.: 24) NH₂-RKREIRLQKNREAAREC-COOH. The peptide was synthesized and coupled to Sulfo-SMCC

20 (Pierce) activated keyhole limpet hemocyanin. The antigen was injected into rabbits (100 µg) and boosted at two week intervals. Sera was bled and tested for immune reactivity towards bacterially-expressed dCREB2-b protein. The antiserum was passed through a CM Affi-gel Blue column

25 (Biorad), and the flow-through was concentrated by ammonium sulfate precipitation, resuspended and dialyzed against PBS (0.14 M NaCl, 2.7 mM KCl, 4.3 mM Na₂HPO₄·7H₂O, 1.4 mM KH₂PO₄, pH 7.3). The dialyzed serum was affinity-purified using a peptide column made using an Ag/Ab Immobilization kit

30 (Immunopure from Pierce). After the antiserum was eluted using a 4M MgCl₂, 0.1 M HEPES pH 6.0 buffer, it was dialyzed into PBS and frozen.

Each data point represents approximately 5 fly heads. Groups of about 25-50 flies were collected and quickly

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frozen on liquid nitrogen until all of the time points had been collected. Heads were isolated resuspended in approximately 200 μ l of 1x Laemmli sample buffer, allowed to thaw and homogenized with a Dounce type B pestle.

- 5 Samples were boiled for 5 minutes, and centrifuged for 10 minutes at room temperature in an Eppendoff microcentrifuge. The supernatants were collected and boiled again just prior to loading onto protein gels. Standard procedures were used to separate equal amounts of
- 10 proteins from each sample on 12% polyacrylamide-SDS gels and to transfer them to PVDF membranes by electroblotting (Ausubel, F., *Current Protocols in Molecular Biology*, John Wiley and Sons, New York, 1994).

- The membranes were blocked for 60 minutes with a 5% BSA solution made up in TBST (10 mM Tris, pH 7.9, 150 mM NaCl, 0.05% Tween 20). The primary antibody was diluted 1:1000 in TBST and incubated with the filter for 30 minutes. The membranes were washed three times with TBST for 5 minutes each time and then incubated for 30 minutes
- 20 with an alkaline phosphatase-conjugated anti-rabbit IgG second antibody (Promega) diluted 1:7500 in TBST. The membranes were washed three more times as before and developed using a chromogenic alkaline phosphatase reaction according to manufacturers suggestions (Promega).

25 Example 3 Transgene Expression Increased After Heat-Shock Induction

In order to interpret the effects of transgene induction on behavior, dCREB2-b expression in transgenic flies (17-2) after heat-shock induction was measured.

- 30 Northern blot analysis revealed elevated levels of hs-dCREB2-b message in the 17-2 flies immediately and three hours after heat-shock (Figure 7A). This induction was also detectable in brain cells using *in situ* hybridization. Western blot showed increased dCREB2-b protein immediately

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after induction (Figure 7B). Elevated levels of the dCREB2-b protein were seen nine hours later and were still detectable twenty four hours after induction. These data indicate that increased amounts of dCREB2-b existed in
5 brain cells throughout spaced training, which ended about six hours after heat induction.

The behavioral experiments also used transgenic flies (A2-2) which expressed a mutated dCREB2-b protein (dCREB2-mLZ). These mutations changed the two internal
10 leucine residues of the leucine zipper to valine residues, and these changes have been shown to result in a protein which is unable to form dimers (Dwarki, V.J. et al., *EMBO J.*, 9: 225-232 (1990)). In transient co-transfection assays, the mutant protein was unable to block
15 PKA-dependent transcription mediated by dCREB2-a, while the wild-type protein had blocking function. Western blot analysis showed that the wild-type and mutant blocker are expressed at similar levels beginning immediately after heat-shock induction and lasting for at least 6 hours
20 (Figure 7C). Therefore, it is unlikely that these two proteins have large differences in expression levels or stability in the transgenic flies.

Northern blot analysis of two different housekeeping genes, *myosin light chain* (Parker, V.P., et al., *Mol. Cell Biol.*, 5: 3058-3068 (1985)) and *elongation factor α*
25 (Hovemann, B., et al., *Nucleic Acids Res.*, 16: 3175-3194 (1988)), showed that steady-state levels of their RNAs were unaffected after transgene induction for at least 3 hours. Gel shift analysis using two different consensus DNA
30 binding sites showed that there was no large effect on the gel shift species which formed after transgene induction for at least 9 hours. Cotransfection of the blocker did not interfere with the activity of a transcription factor from a different family in cell culture. Considered

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together, *hs-dCREB2-b* probably had fairly specific molecular modes of action after induction.

Example 4 Assessment of the Role of CREBs in Long-Term Memory Formation

5 Flies were fed 35 mM cycloheximide (CXM) for 12-14 hours before, or for the 24-hr retention interval immediately after, massed or spaced training (Figure 8). Each of these CXM feeding regimens significantly reduced one-day memory after spaced training but had no effect on
10 one-day memory after massed training (Figure 8). Thus, cycloheximide feeding immediately before or after spaced training disrupts one-day memory. These results suggest that protein synthesis is required soon after training for the formation of long-lasting memory.

15 The results in Figure 8 show that cycloheximide feeding affects one-day retention after spaced training but not massed training. Different groups of wild-type (Can-S) flies were fed 5% glucose solution alone (hatched bars) or laced with 35 mM CXM (striped bars) either for 12-14 hr
20 overnight before massed or spaced training or for the 24-hr retention interval immediately after training. One-day memory retention was significantly lower than normal in flies fed CXM before ($P < 0.001$) or after ($P < 0.001$) spaced training. In both cases, one-day retention in CXM-
25 fed flies was reduced to a level similar to one-day memory after massed training in glucose-fed flies ($P = 0.88$ for CXM before training and $P = 0.71$ for CXM after training). In contrast, no difference was detected between CXM-fed and control flies for one-day memory after massed training ($P =$
30 0.49 and $P = 0.46$, respectively).

One day retention after spaced training was unaffected in uninduced (-hs) transgenic flies (17-2) but was significantly reduced in induced (+hs) transgenic flies (Figure 9A). In contrast, one-day retention after massed

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training was normal in both uninduced and induced transgenic flies (Figure 9A). Comparisons of one-day retention after spaced or massed training between wild-type flies with (+hs) or without (-hs) heat-shock indicated that the heat-shock regimen itself did not have a non-specific effect on memory after either training protocol. Thus induction of the *dCREB2-b* transgene only affected (i.e., disrupted) one-day memory after spaced training.

One day retention after spaced or massed training in *M11-1*, a second line carrying an independent *hs-dCREB2-b* insertion, also was tested. Results with *M11-1* were similar to those obtained with 17-2 (Figure 9B). These results show that the effect of induced *hs-dCREB2-b* does not depend on any particular insertion site of the transgene.

The results in Figures 9A-9C show that induction of the *dCREB2-b* transgene disrupts one-day memory after spaced training, while one-day memory after massed training and learning are normal.

In Figure 9A, different groups of wild-type (Can-S) flies (hatched bars) or *hs-dCREB2-b* transgenic (17-2) flies (striped bars) were given spaced training or massed training in the absence of heat shock (-hs) or three hours after heat shock (+hs). After training, flies were transferred to standard food vials and stored at 18°C until one-day memory was assayed. No differences in one-day memory after spaced or massed training were detected between Can-S vs. 17-2 flies in the absence of heat shock (-hs; $P = 0.83$ and 0.63 , respectively). When flies were trained three hours after heat shock (+hs), however, one-day memory was significantly different between Can-S v. 17-2 flies after spaced training ($P < 0.001$) but not after massed training ($P = 0.23$). In fact, the one-day memory after spaced training was no different than that after massed training in induced 17-2 flies ($P = 0.59$). In

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addition, the heat-shock regimen did not produce a non-specific effect on one-day retention after spaced ($P = 0.59$) or massed ($P = 1.00$) training in Can-S flies. $N=6$ performance indices (PIs) per group.

5 The experiment described in Figure 9A was repeated in Figure 9B with a second, independently derived *dCREB2-b* transgenic line, *M11-1* (striped bars). Here again, a) no differences in one-day memory after spaced or massed training were detected between Can-S vs. *M11-1* flies in the
10 absence of heat-shock (-hs; $P = 0.83$ and 0.86 , respectively), b) a significant difference between Can-S v. *M11-1* for one-day memory after spaced training ($P < 0.001$) but not after massed training ($P = 0.85$) when trained three hours after heat-shock (+hs), c) one-day memory after
15 spaced training was no different than that after massed training in induced *M11-1* flies ($P = 0.43$) and d) the heat-shock regimen did not produce a non-specific effect on one-day retention after spaced ($P = 0.59$) or massed ($P = 0.94$) training in Can-S flies. $N=6$ PIs per group.

20 If induction of the transgene specifically affected LTM via disruption of gene expression, then learning should not be affected, since it does not require new protein synthesis. Different groups of flies were trained using one-cycle training either without heat-shock, or three or
25 twenty four hours after heat-shock. These time points after induction were selected to correspond to the times when flies were trained and tested in the previous experiments (see Figures 9A and 9B). Induction of the transgene (*d-CREB2-b*) in the 17-2 line had no effect on
30 learning in either case (Figure 9C).

 In Figure 9C, different groups of Can-S flies (hatched bars) or 17-2 transgenic flies (striped bars) received one-cycle training in the absence of heat shock (-hs) or three (+hs 3hr) or 24 (+hs 24hr) hours after heat-shock and then
35 were tested immediately afterwards. In each case, no

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differences between Can-S vs. 17-2 flies were detected (P s = 0.28, 0.64 and 0.42, respectively), indicating that learning was normal in induced or uninduced transgenic flies. N=6 PIs per group.

5 Induction of the transgene which contained the mutant blocker (A2-2) did not affect one-day retention after spaced training, while the wild-type blocker (17-2) had a dramatic effect (Figure 10). The *w(iso CJ1)* flies, whose one-day retention also was unaffected by heat induction, is
10 the isogenic control for the mutant blocker transgenic flies. Since Western blot analysis showed that wild-type and mutant blockers probably have similar expression levels, this result suggests that the blocker requires an intact leucine zipper to function effectively.

15 Figure 10 shows that induction of the *hs-dCREB2-mLZ* mutant blocker does not affect one-day retention after spaced training. Different groups of wild-type [*w(iso CJ1)*], *hs-dCREB2-b* transgenic (17-2) or mutant *hs-dCREB2-mLZ* transgenic flies (A2-2) received spaced training in the
20 absence of heat-shock (-hs) or three hours after heat-shock (+hs). The flies were then handled and tested as in Figure 9A. No differences in one-day memory after spaced training were detected between *w(isoCJ1)* vs. 17-2 flies or between
25 *w(isoCJ1)* vs. A2-2 flies in the absence of heat shock (-hs; P = 0.38 and 0.59, respectively). When flies were trained three hours after heat shock (+hs), however, one-day memory after spaced training was significantly different between
30 *w(isoCJ1)* vs. 17-2 flies (P < 0.001) -- as in Figure 9A -- but was not different between *w(isoCJ1)* vs. A2-2 flies (P = 0.78). In addition, the heat-shock regimen did not produce a non-specific effect on one-day retention after spaced training in *w(isoCJ1)* or A2-2 flies (P = 0.40 and P = 0.97, respectively. N=6 performance indices (PIs) per group.

Olfactory acuity and shock reactivity are component
35 behaviors essential for flies to properly learn odor-shock

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associations. The Table shows the scores for these peripheral behaviors for *Can-S* versus 17-2 flies. With or without heat-shock, olfactory acuity and shock reactivity were normal in 17-2 transgenic flies. Thus, *hs-dCREB2-b* induction does not affect olfactory acuity or shock reactivity.

If induction of *hs-dCREB2-b* blocks long-term memory (LTM), then long-lasting memory also should be blocked. In wild-type flies, seven-day retention after spaced training consists solely of the CXM-sensitive LTM because the CXM insensitive ARM component has decayed away. In uninduced transgenic flies (17-2), seven-day retention after spaced training was similar to retention in uninduced wild-type flies ($P = 0.83$; Figure 11). Seven-day retention was severely disrupted, however, in transgenic flies which were trained three hours after heat-shock ($P = 0.001$) and did not differ from zero ($P = 0.91$). In contrast, the heat-shock protocol had no detectable effect on seven-day memory in wild-type flies ($P = 0.39$). Thus, induction of *hs-dCREB2-b* disrupts long-term memory (LTM).

Figure 11 shows that induction of *hs-dCREB2-b* completely abolishes 7-day memory retention. Previous analyses of *radish* mutants indicated that memory retention four or more days after spaced training reflects the sole presence of LTM. Thus, the effect of induced *hs-dCREB2-b* on LTM was verified by comparing 7-day retention after spaced training in *Can-S* (hatched bars) vs. 17-2 transgenic (striped bars) flies that were trained in the absence of heat-shock (-hs) or three hours after heat shock (+hs). Flies were stored in standard food vials at 18°C during the retention interval. $N=6$ PIs per group. Seven-day retention after spaced training did not differ between *Can-S* and 17-2 in the absence of heat-shock ($P = 0.83$) but was significantly lower than normal in 17-2 flies after heat-shock ($P = 0.002$). In fact, 7-day retention after spaced

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training in induced 17-2 transgenic flies was not different from zero ($P = 0.92$). In addition, the heat-shock regimen did not affect 7-day retention after spaced training non-specifically in Can-S flies ($P = 0.39$).

5 If induction of the *hs-dCREB2-b* transgene specifically blocks LTM, then it should only affect the CXM-sensitive component of consolidated memory after spaced training. For both transgenic lines, 17-2 and M11-1, the effect of transgene induction looked similar to the effect that CXM
10 had on wild-type flies (compare Figure 8 with Figures 9A and 9B). This similarity suggested that the induced dCREB2-b protein completely blocked CXM-sensitive memory, leaving ARM intact. The *radish* mutation disrupts ARM (Folkers, E., et al., *Proc.Natl.Acad.Sci. USA*, 90: 8123-
15 8127 (1993)), leaving only LTM one day after spaced training. Thus, a *radish hs-dCREB2-b* "double mutant" (*rsh; 17-2*) was constructed to allow examination of LTM in the absence of ARM. In the absence of heat-shock, *rsh;17-2* double-mutants and *radish* single-gene mutants yielded
20 equivalent one-day retention after spaced training (Figure 12). In contrast, when these flies were heat-shocked three hours before spaced training, one-day retention was undetectable in *rsh;17-2* flies but remained at mutant levels in *radish* flies. The double mutant also showed
25 normal (*radish*-like) learning ($P = 0.59$) and normal (wild-type) olfactory acuity and shock reactivity in the absence of heat-shock versus three hours after heat shock (see the Table).

Figure 12 shows that induction of *hs-dCREB2-b*
30 completely abolishes one-day memory after spaced training in *radish; 17-2* "double mutants." Since *radish* is known to disrupt ARM, a clear view of the effect of *hs-dCREB2-b* on LTM was obtained in *radish;17-2* flies. One-day retention after spaced training was assayed in *rsh;17-2* double
35 mutants and in 17-2 and *rsh* single-gene mutants as

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controls. Flies were trained in the absence of heat-shock (hatched bars) or three hours after heat-shock (striped bars) and stored at 18°C during the retention interval. As usual, induction of *hs-dCREB2-b* produced significantly
5 lower one-day memory after spaced training in 17-2 flies ($P < 0.001$). The heat-shock regimen, however, had no effect on such memory in *radish* mutants

TABLE 1. Olfactory acuity and shock reactivity in Can-S (wild-type), 17-2 (hs-dCREB2-b transgenic) and *rsh*; 17-2 (radish, hs-dCREB2-b "double mutant") flies^a.

Heat Shock	Group	Olfactory Acuity				Shock Reactivity	
		OCT		MCH		60V	20V
		10 ⁰	10 ⁻²	10 ⁰	10 ⁻²		
-hs	CAN-S 17-2	58±3 60±3	32±3 34±8	80±2 77±3	33±7 37±5	79±5 87±3	52±5 43±2
+hs (3 hrs)	CAN-S 17-2	69±4 71±4	41±4 37±3	77±2 76±5	25±9 26±3	74±5 78±3	58±6 67±5
+hs (24 hr)	CAN-S 17-2	66±2 65±3	56±8 42±6	79±4 76±3	33±2 41±5	84±3 85±2	63±3 60±6
-hs	CAN-S <i>rsh</i> ; 17-2	51±4 57±3	39±5 39±5	72±5 74±5	33±7 29±4	87±3 82±4	52±5 53±6
+hs (3 hr)	CAN-S <i>rsh</i> ; 17-2	72±4 68±4	48±3 46±6	66±2 78±2	60±3 49±4	80±4 83±1	58±6 50±5

^a Olfactory acuity and shock reactivity were assayed in untrained flies with the methods of Boynton, S. and T. Tully, Genetics, 131: 655-672 (1992) and Dura, J-M., et al., J. Neurogenet., 9: 1-14 (1993), respectively (see Examples for more details). N=98 PIs per group.

Planned comparisons between Can-S vs. mutant flies failed to detect any significant differences with any heat-shock regimen.

^a10⁰ is manual concentration and corresponds to 10⁻³ for bubbler.

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($P = 0.52$), which reflects only the presence of LTM. In contrast, heat-shock produced significantly lower scores in *rash;17-2* double mutants ($P < 0.001$), which were not different from zero ($P = 0.20$). $N=6$ PIs per group.

5

The following materials and methods were used in the work described in Examples 5 and 6.

Pavlovian Learning and Memory and Testing

10 During one training session, a group of about 100 flies was exposed sequentially to two odors [either octanol (OCT) or methylcyclohexanol (MCH)] for 60 seconds with 45-second rest intervals after each odor presentation. During exposure to the first odor, flies received twelve 1.5-
15 second pulses of 60 V DC with a 5-second interpulse interval.

After training, flies were transferred to food vials and stored at 18°C for a seven-day retention interval. Conditioned odor-avoidance responses then were tested by
20 transferring flies to the choice point of a T-maze, where they were exposed simultaneously to OCT and MCH carried on converging currents of air in the distal ends of the T-maze arms and out the choice point.

Flies were allowed to distribute themselves in the T-maze arms for 120s, after which they were trapped in their
25 respective arms, anesthetized and counted. The "percent correct" then was calculated as the number of flies avoiding the shock-paired odor (they were in the opposite T-maze arm) divided by the total number of flies in both
30 arms. (The number of flies left at the choice point, which usually was less than 5%, were not included in this calculation.) Finally, a performance index (PI) was calculated by averaging the percent corrects of two reciprocal groups of flies -- one where OCT and shock were
35 paired, the other where MCH and shock were paired--and then

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by normalizing the average so that a PI=0 represented a 50:50 distribution in the T-maze and a PI=100 represented 100% avoidance of the shock-paired odor.

All behavioral experiments were designed in a balanced fashion with N=2 PIs per group collected per day; then replicated across days to generate final Ns. In all experiments, the experimenter was blind to genotype.

Statistical Analyses of Behavior Data

PIs are distributed normally (Tully, T. and D. Gold, *J. Neurogenet.*, 9: 55-71 (1993)). Consequently, untransformed (raw) data were analyzed parametrically with JMP3.01 statistical software (SAS Institute Inc., Cary NC). Negative accelerating exponential Gompertz (growth) functions (see Lewis, D., *Quantitative Methods in Psychology*, McGraw-Hill, New York, New York (1960)) were fit to the data in Figures 13A and 13B via nonlinear least squares with iteration.

Example 5 Effect on Long Term Memory of Repeated Training Sessions

Seven-day memory retention (a measure of long term memory) in wild-type (Can-S) flies is induced incrementally by repeated training sessions. An automated version of a discriminative classical conditioning procedure was used to electroshock flies during exposure to one odor (CS+) but not to a second odor (CS-). Seven days after one or more training sessions, memory retention of conditioned odor avoidance responses was quantified in a T-maze, where flies were presented the CS+ and CS- simultaneously for 120 seconds.

In Figure 13A, long term memory as a function of the number of training sessions is indicated by open circles. One training session produced a mean performance index (PI \pm SEM; Note 1) near zero. Additional training sessions

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with a 15-minute rest interval between each, however, yielded a steady increase in mean PIs with a maximum of 39 after ten training sessions. Ten additional training sessions produced similar performance. A nonlinear "growth" function (solid line) was fit to the individual PIs using an iterative least squares method. N = 13, 6, 6, 6, 13, 7, 7, 7, 6, 7 and 7 PIs for groups receiving 1-10, 15 and 20 training sessions, respectively.

10 Example 6 Effect on Long Term Memory of the Rest
 Interval Between Each Training Session

Seven-day memory retention (a measure of long term memory) in wild-type (Can-S) flies is induced incrementally by the rest interval between each training session. As described in Example 5, an automated version of a discriminative classical conditioning procedure was used to electroshock flies during exposure to one odor (CS+) but not to a second odor (CS-). Seven days after one or more training sessions, memory retention of conditioned odor avoidance responses was quantified in a T-maze, where flies were presented the CS+ and CS- simultaneously for 120 seconds.

In Figure 13B, long term memory as a function of the rest interval is indicated by open circles. Ten training sessions with no rest interval between each (massed training) produced a mean PI near zero. Increasing the rest interval between each of ten training sessions yielded a steady increase in mean PIs with a maximum of 34 for a 10-minute rest interval. Rest intervals up to ten minutes longer produced similar performance. A nonlinear growth function (solid line) was fit to the data as above. N = 12, 6, 6, 6, 6, 13, 7, 7, 7, 7, 7, 7 and 7 PIs for groups receiving 0-10, 15 and 20 minutes of rest between each training session.

35

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The following materials and methods were used in the work described in Examples 7-10.

Isolating Transgenic Flies

5 EcoRI restriction sites were added (using PCR) just 5' to the putative translation initiation site and just 3' to the translation termination site in the *dCREB2-a* cDNA. This fragment was sequenced and subcloned into CaSpeR hs43, a mini-white transformation vector which contains the *hsp70* promoter, in the orientation so that the *dCREB2-a* open reading frame is regulated by the *hsp70* promoter. Germ-line transformation was accomplished by injecting into isogenic *w(isoCJ1)* embryos using standard techniques (Spradling, A.C. and G.M. Rubin, *Science*, 218: 341-347 (1982); Rubin, G.M. and A. Spradling, *Science*, 218: 348-353 (1982)). By injecting DNA into the relatively homogeneous genetic background of *w(isoCJ1)*, outcrossing of the resulting germ-line transformants to equilibrate (heterogeneous) genetic backgrounds was not necessary. Two transgenic lines, C28 and C30, each with one independent P-element insertion were generated and characterized. They appeared normal in general appearance, fertility and viability. Flies homozygous for the C28 or C30 transgene were bred and used for all experiments.

25

Heat Shock Regimen

For heat-shock induction, flies were collected within two days of eclosion, placed in glass bottles in groups of about 600, and incubated overnight at 25°C and 70% relative humidity. The next day, three hours before training, groups of approximately 100 flies were transferred to foam-stoppered glass shell vials containing a strip of filter paper to absorb excess moisture. The vials then were submerged in a 37°C water bath until the bottom of the foam stopper (inside the vial) was below the surface of the

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water, thereby insuring that the flies could not escape heat-shock. The vial remained submerged for 30 minutes, after which the flies were transferred to a standard food vial for a 3-hr recovery period at 25°C and 70% relative humidity. Training began immediately after the recovery period.

Statistical Analyses of Behavior Data

PIs from the three strains (Can-S, C28 and C30) and six training-regiments (1x+hs, 2xmassed+hs, 10xmassed+hs, 1x-hs, 2xmassed-hs and 10xmassed-hs) were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(2, 102)}=48.34$; $P < 0.001$) and TRAINING-regimen ($F_{(5, 102)}=25.47$, $P < 0.001$) as main effects and STRAIN x TRAIN ($F_{(10, 102)}=5.85$, $P < 0.001$) as the interaction term. Since preliminary experiments preceded all of the experiments summarized herein, all pairwise comparisons were planned. To maintain an experimentwise error rate of $\alpha = 0.05$, the individual comparisons summarized in Figure 15B were judged significant if $P < 0.002$ (Sokal, R.R. and F.J. Rohlf, *Biometry*, 2nd Edition, W.H. Freeman and Company, New York (1981)).

Example 7 A Molecular Switch for the Formation of Long Term Memory

Figure 14 presents a conceptual method of a molecular switch for the formation of LTM, based on differential regulation of CREB isoforms with opposing functions.

Immediately after one training session, the relevant CREB activators and repressors are induced. Their combined functions (rather than molecular concentrations) are equivalent and yielded no net effect of CREB activators. Thus, repeated sessions of massed training (no rest interval) never induce LTM (see Figure 15A). CREB repressors functionally inactivate faster than CREB activators, however, yielding an increasing net effect of

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CREB activators (ΔC) with time (see Figure 13B). If ΔC is positive at the end of a particular rest interval during spaced training, then CREB activators are free to initiate downstream events involved with the formation of LTM.

- 5 Usually, ΔC after one training session is not large enough to yield much LTM. Thus, repeated spaced training sessions serve to increase ΔC incrementally eventually to produce maximal LTM (see Figure 13A).

Experimental verification of two predictions from this
10 model involving CREB as a molecular switch for long term memory formation is shown in Figures 15A-15C and discussed in Examples 8-10.

15 Example 8 Effect on Long Term Memory of Having Equal
Amounts of CREB Activators and Repressors
Immediately After One Training Session

The model of a molecular switch for LTM predicts that the functional effects of all CREB activators and repressors are equal immediately after one training session
20 ($\Delta C=0$). If no rest interval occurred between additional training sessions (massed training), then functional CREB activator would not accumulate, thereby preventing the induction of downstream events required for LTM induction.

To test this notion, wild-type (Can-S) flies were
25 subjected to 48, instead of the usual 10 (see Figure 15B), massed training sessions (48x massed) or, as a positive control, to 10 spaced training sessions with a 15-minute rest interval (10x spaced). Seven-day memory after such massed training was near zero (Figure 15A), while that
30 after spaced training was near its usual maximum value (see Figure 13A). Thus, nearly five times the usual amount of massed training still did not induce LTM. N=6 PIs for each group.

PIs from two groups (10x spaced or 48x massed) of
35 wild-type (Can-S) files were subjected to a ONE-WAY ANOVA

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with GROUP ($F_{(10)}=51.13$; $P < 0.001$) as the main effect. A subsequent planned comparison revealed that the mean PI of the 48x massed group did not differ significantly from zero ($t_{(10)}=1.66$; $P=0.127$).

5

Example 9 Effect on Long Term Memory of Increasing Amounts of CREB Activator

The model of a molecular switch for LTM predicts that experimentally increasing the amount of CREB activator will
10 eliminate the requirements for at least 10 repeated training sessions with a 10-minute rest interval between each to produce maximal LTM.

To test this idea, two transgenic lines (C28 and C30) carrying an inducible *hsp-dCREB2-a* activator construct
15 inserted into different cytological locations were generated. Different groups of flies from these two transgenic lines were subjected, along with wild-type (Can-S) flies, to 1 (1x) 2 (2x) or (10x) massed training sessions three hours after heat-shock induction of the
20 transgene (induced) or in the absence of heat-shock (uninduced).

Without heat-shock, seven-day memory in all three strains did not differ from zero after one, two or ten massed training sessions (all $P_s > 0.002$). With heat-
25 shock, seven-day memory in wild-type flies remained near zero in each massed training group (all $P_s > 0.002$). In contrast, seven-day memory was significant (near the maximum of 35) after ten massed sessions in both the C28 and C30 transgenic lines (all $P_s < 0.0001$). Moreover,
30 seven-day memory after one training session was similar to that after ten training sessions in both C28 ($P = 0.89$) and C30 ($P = 0.89$) transgenic flies. Thus, maximum LTM was induced after just one training session in transgenic flies expressing abnormally high levels of CREB activator. $N=10$,

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4 and 6 PIs for each group of Can-S, C28 and C30, respectively.

Example 10 Olfactory Acuity and Shock Reactivity

5 Odor avoidance responses to OCT or to MCH were quantified with the method of Boynton, S. and T. Tully, *Genetics*, 131: 655-672 (1992), given a choice between an odor and air. The odors are naturally aversive, and flies usually chose air and avoided the T-maze arm containing the
10 odor. After 120 seconds, the flies were trapped in their respective arms of the T-maze, anesthetized and counted. A PI was calculated as a normalized percent correctly avoiding the odor (cf. Example 5). PIs from these two strains and two odor-groups (OCT and MCH) were subjected to
15 a TWO-WAY ANOVA with STRAIN ($F_{(1, 12)}=1.57$, $P=0.23$) and ODOR ($F_{(1, 12)}=0.07$, $P=0.80$) as main effects and DRUGxODOR ($F_{(1, 12)}=0.15$, $P=0.71$) as the interaction term. The two subsequent planned comparisons were judged significant if $P < 0.025$.

20 Shock reactivity was quantified with the method of Dura, J-M., et al., *J. Neurogenet.*, 9: 1-14 (1993) in wild-type (Can-S) flies, or in a transgenic line (C28) carrying an inducible *hsp-dCREB2-a* construct, three hours after a 30-minute heat shock at 37°C. Briefly, flies were placed
25 in a T-maze and given a choice between an electrified grid (60V DC) in one T-maze arm and an unconnected grid in the other. After 120 seconds, the flies were trapped in their respective T-maze arms, anesthetized and counted. A PI was calculated as for olfactory acuity. PIs from these two
30 strains were subjected to a ONE- WAY ANOVA with STRAIN ($F_{(1, 6)}=13.03$, $P=0.01$) as the main effect.

Naive avoidance responses to odors or to shock three hours after heat-shock did not differ between wild-type (Can-S) versus transgenic (C28) flies for the two odorants
35 (MCH and OCT) used for conditioning experiments ($P=0.27$,

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0.55, respectively). N=4 PIs per group. Naive shock avoidance responses three hours after training for transgenic flies were slightly lower than those for wild-flies (P=0.01). N=4 PIs per group.

5

Examples 11-13 pertain to the *Drosophila* nitric oxide synthase work.

10 Example 11 Low Stringency Hybridization to a Phage
 Library of the *Drosophila* Genome and
 Screening of *Drosophila* cDNA Library

6x10⁴ plaques of a genomic *Drosophila* λDASH library with the 1.3 kb Bgl II fragment of rat neuronal NOS cDNA (residues 3282-4573) under low stringency conditions of 40%
15 formamide were screened as described in W.M. McGinnis et al., *Nature* 308: 428 (1984). Fifty positive phage were purified and grouped based on inter se hybridization. The contig containing the 2.4R fragment of dNOS was comprised of 15 phage clones. Regions of cross-hybridization to the
20 rat probe were identified, subcloned and three of them were sequenced. The other two did not contain sequences homologous to any protein in the database. A *Drosophila* head cDNA library (a gift from P. Salvaterra) was screened with the 2.4R fragment isolated from phage clone λ8.11 in
25 standard conditions. All phage purification and cloning steps were done with standard methods (J. Sambrook, E.F. Fritsch, T. Maniatis, *Molecular cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989)). cDNA fragments were subcloned into Bluescript
30 (Stratagene) and sequenced on both strands with Sequenase 2.0 (USB).

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Example 12 Activity of *Drosophila* Nitric Oxide Synthase
(dNOS)

The expression construct for activity assays contained dNOS cDNA (with an XbaI site engineered immediately
5 upstream of the ATG codon) cloned into the XbaI and SmaI sites of the pCGN expression vector [M. Tanaka and W. Herr, *Cell*, 60: 375 (1990)]. 293 human kidney cells were transfected with 15µg of the dNOS construct, or vector DNA, and precipitated with calcium phosphate as described in
10 [M.J. Imperiale, L.T. Feldman and J.R. Nevins, *Cell*, 35: 127 (1983)]. Cells were collected 2 days later and protein extracts were prepared as described in [J. Sambrook, E.F. Fritsch, T. Maniatis, *Molecular cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory, Cold Spring Harbor,
15 NY, 1989)].

The fusion protein for raising anti-DNOS antibodies was made by cloning a 0.29 kb Eam1105I-SacI fragment of dNOS cDNA (this fragment codes for 97 N-terminal amino acids of dNOS ORF) into EcoRI site of pGEX-KG [K. Guan and
20 J.E. Dixon, *Anal. Biochem.*, 192: 262 (1991)]. The fusion protein was expressed in BL21 *E. coli* strain and purified over Glutathione-Sepharose columns (Pharmacia) as described in [G.J. Hannon, D. Demetrick, D. Beach, *Genes & Dev.*, 7: 2378 (1993)]. Immunization of rabbits, and serum
25 preparation, was done by Hazleton Research Products, Inc. (Denver). The DNOS protein was detected on Western blots using a 1:500 dilution of rabbit serum, and cross-reacting bands were visualized with anti-rabbit alkaline phosphatase conjugate (Promega) according to the protocol provided.

30 The enzymatic assay was done essentially as described previously (D. Bredt and S. Snyder, *Proc. Natl. Acad. Sci. USA*, 87: 682 (1990)]. A 100 ml reaction mixture containing 25 µl (50-100 µg) of soluble protein extract, 50 mM Hepes, pH 7.4, 3 µM FAD, 3µM FMN, 10 µM tetrahydrobiopterin (ICN),
35 1 mM DTT, .8 mM CaCl₂, 1 mM NADPH, 10 µg/ml calmodulin, 2µl

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of [^3H]L-arginine (35.7 Ci/mmol, NEN) and 50 mM L-valine in was incubated for 60 minutes at 37°C. The reaction was stopped with 0.5 ml 20 mM Hepes pH 5.5, 2mM EDTA, 2mM EGTA, loaded on 0.5 ml Dowex AG 50WX-8 (Na^+ form) column and
5 eluted with 3x0.5 ml of the stop buffer. Radioactivity present in the eluent was quantified in a scintillation counter.

Figures 17A-17B show the expression of DNOS enzymatic activity in 293 kidney cells. Figure 17A shows the results
10 of a Western blot analysis of protein extracts from 293 cells transfected with vector alone (lane 293 + vector) or with *dnOS* cDNA construct (lane 293 + *dnOS*). 25 μg of soluble protein extracts was resolved on 7.5% polyacrylamide gel, transferred to nitrocellulose membrane
15 and treated with anti-DNOS antibody. The arrow indicates the position of the DNOS protein. Positions of molecular weight markers (in kD) are shown on the left.

Figure 17B shows significant DNOS enzyme activity measured in 293 cell extracts by conversion of ^3H -L-
20 arginine to ^3H -L-citrulline. Enzymatic activity was detected only in cells transfected with *dnOS* cDNA construct (groups B-D) and is presented as specific activity (pmol of citrulline/mg/min.). The DNOS activity also was measured in the presence of 1 mM EGTA without exogenous Ca^{2+} or
25 calmodulin (group C), or in the presence of 100 mM L-NAME (group D). N=4 reactions per group.

Example 13 Splicing Pattern of *dnOS*

Heads and bodies of adult flies were separated on
30 sieves. Total RNA was isolated by the guanidinium isothiocyanate method [P. Chomczynski and N. Sacchi, *Anal. Biochem.*, 162: 156 (1987)]. Poly(A) $^+$ RNA selection, Northern blot and hybridization were done with standard methods (J. Sambrook, E.F. Fritsch, T. Maniatis, *Molecular*
35 *cloning: A Laboratory Manual* (Cold Spring Harbor

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Laboratory, Cold Spring Harbor, NY, 1989)]. The blot was hybridized with random-primed dNOS cDNA (10^6 cpm/ml), washed in 0.1xSSC and 0.1% SDS at 65°C and exposed to X-ray film for 72 hours. Two 25-mer primers [corresponding to
5 residues 1374-1399 (the top primer) and 1793-1817 (the bottom primer) in the dNOS sequence] were used to amplify fragments of two dNOS splice products. Each RT-PCR reaction contained 30 ng of poly(A)⁺ head RNA. In the first stage (RT), 90 ng of the bottom primer and 5U of rTth
10 polymerase (Perkin-Elmers) were added and the mixture was incubated in the MJ Research Minicycler[®] in the following sequence of conditions: 95°C/1 minute, 67°C/45 seconds, 70°C/13 minutes. The second stage (PCR) was carried out as follows: 94°C/45 seconds, 63°C/45 seconds, 70°C/90 seconds
15 and was repeated for 35 cycles. Products of the reaction were analyzed on a denaturing polyacrylamide (8%) gel. Bands of interest were isolated, reamplified, cloned into pCR1000 (InVitrogen) and sequenced with Sequenase kit (USB).

20 Northern blot analysis of dNOS expression in adult flies shows a 5.0 kb dNOS transcript present in heads (Figure 18A). Each lane contained 10 mg of poly (A)⁺ mRNA isolated from *Drosophila* heads (H) or bodies (B). The Northern blot was hybridized with the dNOS cDNA as
25 described above. Positions of size markers (in kb) are shown on the left. The blot was overprobed with myosin light chain (MLC) (Parker, V.P., Mol. Cell Biol. 5: 3058-3068 (1985)) as a standard for RNA concentration.

Figure 18B shows that the dNOS gene expresses two
30 alternatively spliced mRNA species. RT-PCR reactions were performed on poly(A)⁺ mRNA isolated from *Drosophila* heads and were resolved on 8% polyacrylamide gel. Arrows indicate the positions of DNA fragments of expected sizes: the 444 bp long-form fragment and the 129 bp short-form
35 fragment (lane +RNA). Other bands present in this lane are

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artifacts from heteroduplexes that failed to denature.
Poly(A)⁺ mRNA was omitted from the control reaction (lane
-RNA), which otherwise was done in identical conditions.
Size markers (kb ladder) are shown in the middle lane (KB).

5

Equivalents

Those skilled in the art will know, or be able to
ascertain, using no more than-routine experimentation, many
equivalents to the specific embodiments of the invention
10 described herein. These and all other equivalents are
intended to be encompassed by the following claims.

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ASSOCIATED WITH LONG-TERM MEMORY

(iii) NUMBER OF SEQUENCES: 25

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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-95-

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1083 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "cDNA and PCR analysis"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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1 5 10 15	
GGC TCC AAT GAC GTG GTC GAT GTC GTT GCC CAA CAG GCG GCG GCA GCG	96
Gly Ser Asn Asp Val Val Asp Val Val Ala Gln Gln Ala Ala Ala Ala	
20 25 30	
GTG GGC GGC GGC GGT GGA GGA GGA GGA GGC GGC GGC GGC GGT GGT AAC	144
Val Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn	
35 40 45	
CCC CAG CAG CAG CAA CAG AAC CCA CAA AGT ACA ACG GCC GGC GGT CCA	192
Pro Gln Gln Gln Gln Gln Asn Pro Gln Ser Thr Thr Ala Gly Gly Pro	
50 55 60	
ACG GGT GCG ACG AAC AAC GCC CAG GGA GGC GGA GTG TCC TCC GTG CTG	240
Thr Gly Ala Thr Asn Asn Ala Gln Gly Gly Gly Val Ser Ser Val Leu	
65 70 75 80	
ACC ACC ACC GCC AAC TGC AAC ATA CAA TAC CCC ATC CAG ACG CTG GCG	288
Thr Thr Thr Ala Asn Cys Asn Ile Gln Tyr Pro Ile Gln Thr Leu Ala	
85 90 95	
CAG CAC GGA CTG CAG GTG AGC ATT TGG GGA CCG GGT GCT TGG TGT CAA	336
Gln His Gly Leu Gln Val Ser Ile Trp Gly Pro Gly Ala Trp Cys Gln	
100 105 110	

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CTG	TCG	AGT	GTC	AGG	TGT	TAC	GGA	TCC	CAG	CCA	GAA	GTG	GCT	ACC	AAG	384
Leu	Ser	Ser	Val	Arg	Cys	Tyr	Gly	Ser	Gln	Pro	Glu	Val	Ala	Thr	Lys	
		115					120					125				
GAT	GTG	CAG	TCC	GTG	ATA	CAG	GCC	AAT	CCC	TCG	GGA	GTC	ATA	CAG	ACA	432
Asp	Val	Gln	Ser	Val	Ile	Gln	Ala	Asn	Pro	Ser	Gly	Val	Ile	Gln	Thr	
	130					135					140					
GCA	GCT	GGA	ACC	CAG	CAG	CAG	CAA	CAG	GCG	CTG	GCC	GCC	GCC	ACA	GCG	480
Ala	Ala	Gly	Thr	Gln	Gln	Gln	Gln	Gln	Ala	Leu	Ala	Ala	Ala	Thr	Gln	
145					150					155					160	
ATG	CAG	AAG	GTG	GTC	TAC	GTG	GCC	AAG	CCG	CCG	AAC	TCG	ACG	GTC	ATC	528
Met	Gln	Lys	Val	Val	Tyr	Val	Ala	Lys	Phe	Pro	Asn	Ser	Thr	Val	Ile	
				165					170					175		
CAC	ACG	ACG	CCT	GGC	AAT	GCA	GTG	CAA	GTG	CGT	AAC	AAA	ATC	CCT	CCA	576
His	Thr	Thr	Pro	Gly	Asn	Ala	Val	Gln	Val	Arg	Asn	Lys	Ile	Pro	Pro	
			180					185					190			
ACC	TTT	CCA	TGT	AAG	ATC	AAG	CCC	GAA	CCG	AAC	ACG	CAG	CAC	CCG	GAG	624
Thr	Phe	Pro	Cys	Lys	Ile	Lys	Pro	Glu	Pro	Asn	Thr	Gln	His	Pro	Glu	
		195					200					205				
GAC	AGC	GAC	GAG	AGT	CTG	TCG	GAC	GAC	GAT	TCC	CAG	CAC	CAC	CGC	AGC	672
Asp	Ser	Asp	Glu	Ser	Leu	Ser	Asp	Asp	Asp	Ser	Gln	His	His	Arg	Ser	
	210					215					220					
GAG	CTG	ACG	CGA	CGG	CCG	TCG	TAC	AAT	AAG	ATC	TTC	ACC	GAG	ATC	AGC	720
Glu	Leu	Thr	Arg	Arg	Pro	Ser	Tyr	Asn	Lys	Ile	Phe	Thr	Glu	Ile	Ser	
225					230					235					240	
GGT	CCG	GAC	ATG	AGC	GGC	GCA	TCG	CTT	CCC	ATG	TCC	GAC	GGC	GTG	CTC	768
Gly	Pro	Asp	Met	Ser	Gly	Ala	Ser	Leu	Pro	Met	Ser	Asp	Gly	Val	Leu	
				245					250					255		
AAT	TCC	CAG	CTG	GTG	GGG	ACC	GGA	GCG	GGG	GGC	AAT	GCG	GCG	AAC	AGC	816
Asn	Ser	Gln	Leu	Val	Gly	Thr	Gly	Ala	Gly	Gly	Asn	Ala	Ala	Asn	Ser	
			260					265					270			
TCC	CTG	ATG	CAA	TTG	GAT	CCC	ACG	TAC	TAC	CTG	TCC	AAT	CGG	ATG	TCC	864
Ser	Leu	Met	Gln	Leu	Asp	Pro	Thr	Tyr	Tyr	Leu	Ser	Asn	Arg	Met	Ser	
		275					280						285			
TAC	AAC	ACC	AAC	AAC	AGC	GGG	ATA	GCG	GAG	GAT	CAG	ACC	CGT	AAG	CGC	912
Tyr	Asn	Thr	Asn	Asn	Ser	Gly	Ile	Ala	Glu	Asp	Gln	Thr	Arg	Lys	Arg	
	290					295					300					
GAG	ATC	CGG	CTG	CAG	AAG	AAC	AGG	GAG	GCG	GCG	CGT	GAG	TGC	CGG	CGC	960
Glu	Ile	Arg	Leu	Gln	Lys	Asn	Arg	Glu	Ala	Ala	Arg	Glu	Cys	Arg	Arg	
305					310					315					320	
AAG	AAG	AAG	GAG	TAC	ATC	AAG	TGC	CTG	GAG	AAT	CGA	GTG	GCG	GTG	CTA	1008
Lys	Lys	Lys	Glu	Tyr	Ile	Lys	Cys	Leu	Glu	Asn	Arg	Val	Ala	Val	Leu	
				325					330					335		
GAG	AAC	CAA	AAC	AAA	GCG	CTC	ATC	GAG	GAG	CTG	AAG	TCG	CTC	AAG	GAG	1056
Glu	Asn	Gln	Asn	Lys	Ala	Leu	Ile	Glu	Glu	Leu	Lys	Ser	Leu	Lys	Glu	
			340					345					350			

-97-

CTC TAT TGT CAG ACC AAG AAC GAT TGA
 Leu Tyr Cys Gln Thr Lys Asn Asp
 355 360

1083

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Asn Ser Ile Val Glu Glu Asn Gly Asn Ser Ser Ala Ala Ser
 1 5 10 15
 Gly Ser Asn Asp Val Val Asp Val Val Ala Gln Gln Ala Ala Ala Ala
 20 25 30
 Val Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn
 35 40 45
 Pro Gln Gln Gln Gln Gln Asn Pro Gln Ser Thr Thr Ala Gly Gly Pro
 50 55 60
 Thr Gly Ala Thr Asn Asn Ala Gln Gly Gly Gly Val Ser Ser Val Leu
 65 70 75 80
 Thr Thr Thr Ala Asn Cys Asn Ile Gln Tyr Pro Ile Gln Thr Leu Ala
 85 90 95
 Gln His Gly Leu Gln Val Ser Ile Trp Gly Pro Gly Ala Trp Cys Gln
 100 105 110
 Leu Ser Ser Val Arg Cys Tyr Gly Ser Gln Pro Glu Val Ala Thr Lys
 115 120 125
 Asp Val Gln Ser Val Ile Gln Ala Asn Pro Ser Gly Val Ile Gln Thr
 130 135 140
 Ala Ala Gly Thr Gln Gln Gln Gln Gln Ala Leu Ala Ala Ala Thr Ala
 145 150 155 160
 Met Gln Lys Val Val Tyr Val Ala Lys Pro Pro Asn Ser Thr Val Ile
 165 170 175
 His Thr Thr Pro Gly Asn Ala Val Gln Val Arg Asn Lys Ile Pro Pro
 180 185 190
 Thr Phe Pro Cys Lys Ile Lys Pro Glu Pro Asn Thr Gln His Pro Glu
 195 200 205
 Asp Ser Asp Glu Ser Leu Ser Asp Asp Asp Ser Gln His His Arg Ser
 210 215 220
 Glu Leu Thr Arg Arg Pro Ser Tyr Asn Lys Ile Phe Thr Glu Ile Ser
 225 230 235 240

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Gly	Pro	Asp	Met	Ser	Gly	Ala	Ser	Leu	Pro	Met	Ser	Asp	Gly	Val	Leu
				245					250					255	
Asn	Ser	Gln	Leu	Val	Gly	Thr	Gly	Ala	Gly	Gly	Asn	Ala	Ala	Asn	Ser
			260					265					270		
Ser	Leu	Met	Gln	Leu	Asp	Pro	Thr	Tyr	Tyr	Leu	Ser	Asn	Arg	Met	Ser
		275					280					285			
Tyr	Asn	Thr	Asn	Asn	Ser	Gly	Ile	Ala	Glu	Asp	Gln	Thr	Arg	Lys	Arg
	290					295					300				
Glu	Ile	Arg	Leu	Gln	Lys	Asn	Arg	Glu	Ala	Ala	Arg	Glu	Cys	Arg	Arg
305					310					315					320
Lys	Lys	Lys	Glu	Tyr	Ile	Lys	Cys	Leu	Glu	Asn	Arg	Val	Ala	Val	Leu
				325					330					335	
Glu	Asn	Gln	Asn	Lys	Ala	Leu	Ile	Glu	Glu	Leu	Lys	Ser	Leu	Lys	Glu
			340					345					350		
Leu	Tyr	Cys	Gln	Thr	Lys	Asn	Asp								
		355					360								

(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Lys Arg Glu Ile Arg Leu Gln Lys Asn Arg Glu Ala Ala Arg Glu
1 5 10 15
Cys Arg Arg Lys Lys Lys Glu Tyr Ile Lys Cys Leu Glu Asn Arg Val
20 25 30
Ala Val Leu Glu Asn Gln Asn Lys Ala Leu Ile Glu Glu Leu Lys Ser
35 40 45
Leu Lys Glu Leu Tyr Cys
50

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Arg Lys Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu
1           5           10           15
Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val
20           25           30
Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala
35           40           45
Leu Lys Asp Leu Tyr Cys
50

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Arg Lys Arg Glu Leu Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu
1           5           10           15
Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val
20           25           30
Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala
35           40           45
Leu Lys Asp Leu Tyr Cys
50

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Leu Lys Arg Glu Ile Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu
1           5           10           15
Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val
20           25           30
Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Thr
35           40           45

```

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Leu Lys Asp Leu Tyr Ser
50

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG TTA CTC GGA GAA AAT ATG TTT TCT ACT TTC ACA TCG TTA GAT GCT	48
Met Leu Leu Gly Glu Asn Met Phe Ser Thr Phe Thr Ser Leu Asp Ala	
1 5 10 15	
GCT ACC GCT ACA ACC AAC ACC GGT GAA TTC TTA ATG AAT GAA TCT CCA	96
Ala Thr Ala Thr Asn Thr Gly Glu Phe Leu Met Asn Glu Ser Pro	
20 25 30	
AGG CAA GAA GCC GGT GAC TTA ATG TTG GAT AGT CTG GAT TTC AAC ATT	144
Arg Gln Ala Gly Asp Leu Met Leu Asp Ser Leu Asp Phe Asn Ile	
35 40 45	
ATG GGC GAA AAC CTG GCA GAT GAT TTC CAG ACC TCG GCT TCA CCA GCT	192
Met Gly Glu Asn Leu Ala Asp Asp Phe Gln Thr Ser Ala Ser Pro Ala	
50 55 60	
TCG GAG GAC AAG ATG ACT CCT TTC GTT GTT GAT ACC AAT GTT TTT GAA	240
Ser Glu Asp Lys Met Thr Pro Phe Val Val Asp Thr Asn Val Phe Glu	
65 70 75 80	
TCC GTC TTC AAG AAC ACC GAA GAT ACC CTT CTA GGA GAT ATC GAC AAT	288
Ser Val Phe Lys Asn Thr Glu Asp Thr Leu Leu Gly Asp Ile Asp Asn	
85 90 95	
GTT GGT ATT GTT GAC ACG GAG TTG AAG GAG ATG TTC GAT TTG GTT GAC	336
Val Gly Ile Val Asp Thr Glu Leu Lys Glu Met Phe Asp Leu Val Asp	
100 105 110	
TCG GAA ATC AAT AAC GGC ACT CCT ATC AAG CAG GAA GAA AAG GAT GAT	384
Ser Glu Ile Asn Asn Gly Thr Pro Ile Lys Gln Glu Glu Lys Asp Asp	
115 120 125	
TTG GAA TTT ACT TCA AGA TCC CAG TCC ACC TCA GCT CTC TTG TCG TCG	432
Leu Glu Phe Thr Ser Arg Ser Gln Ser Thr Ser Ala Leu Leu Ser Ser	
130 135 140	
AAA TCG ACT TCT GCT TCT CCA GCT GAT GCT GCC GCT GCA TGT GCA AGT	480
Lys Ser Thr Ser Ala Ser Pro Ala Asp Ala Ala Ala Ala Cys Ala Ser	
145 150 155 160	

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CCT	TCG	TCA	TCG	TCT	TGT	AAA	AGA	TCC	TAT	TCT	TCT	GCT	CAG	CTA	GAA	528
Pro	Ser	Ser	Ser	Ser	Cys	Lys	Arg	Ser	Tyr	Ser	Ser	Ala	Gln	Leu	Glu	
				165					170					175		
ACT	ACG	GGT	TCG	GAT	GCT	CCA	AAG	AAA	GAT	AAG	CTG	GGC	TGC	ACC	CCT	576
Thr	Thr	Gly	Ser	Asp	Ala	Pro	Lys	Lys	Asp	Lys	Leu	Gly	Cys	Thr	Pro	
			180					185					190			
TAC	ACT	AGA	AAA	CAG	AGA	AAC	AAT	CCA	TTA	CCT	CCG	GTC	ATT	CCA	AAG	624
Tyr	Thr	Arg	Lys	Gln	Arg	Asn	Asn	Pro	Leu	Pro	Pro	Val	Ile	Pro	Lys	
			195				200					205				
GGT	CAG	GAT	GTT	GCT	TCT	ATG	AAA	AGG	GCA	AGA	AAC	ACT	GAG	GCC	GCA	672
Gly	Gln	Asp	Val	Ala	Ser	Met	Lys	Arg	Ala	Arg	Asn	Thr	Glu	Ala	Ala	
	210					215					220					
AGA	AGA	TCA	AGA	GCC	AGA	AAA	ATG	GAA	AGA	ATG	TCC	CAA	CTT	GAA	GAA	720
Arg	Arg	Ser	Arg	Ala	Arg	Lys	Met	Glu	Arg	Met	Ser	Gln	Leu	Glu	Glu	
225					230				235					240		
AAG	TGT	CAA	AGC	TTG	TTG	AAG	GAA	AAC	GAC	GAC	TTG	AAA	GCT	CAA	GTT	768
Lys	Cys	Gln	Ser	Leu	Leu	Lys	Glu	Asn	Asp	Asp	Leu	Lys	Ala	Gln	Val	
				245					250					255		
CAA	GCT	TTG	AAG	AAA	TTA	CTT	GGA	CAA	CAA							798
Gln	Ala	Leu	Lys	Lys	Leu	Leu	Gly	Gln	Gln							
			260					265								

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Leu	Leu	Gly	Glu	Asn	Met	Phe	Ser	Thr	Phe	Thr	Ser	Leu	Asp	Ala	
1				5					10					15		
Ala	Thr	Ala	Thr	Thr	Asn	Thr	Gly	Glu	Phe	Leu	Met	Asn	Glu	Ser	Pro	
			20					25					30			
Arg	Gln	Glu	Ala	Gly	Asp	Leu	Met	Leu	Asp	Ser	Leu	Asp	Phe	Asn	Ile	
		35				40						45				
Met	Gly	Glu	Asn	Leu	Ala	Asp	Asp	Phe	Gln	Thr	Ser	Ala	Ser	Pro	Ala	
	50					55					60					
Ser	Glu	Asp	Lys	Met	Thr	Pro	Phe	Val	Val	Asp	Thr	Asn	Val	Phe	Glu	
	65				70				75						80	
Ser	Val	Phe	Lys	Asn	Thr	Glu	Asp	Thr	Leu	Leu	Gly	Asp	Ile	Asp	Asn	
			85					90						95		
Val	Gly	Ile	Val	Asp	Thr	Glu	Leu	Lys	Glu	Met	Phe	Asp	Leu	Val	Asp	
			100					105						110		

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Ser Glu Ile Asn Asn Gly Thr Pro Ile Lys Gln Glu Glu Lys Asp Asp
 115 120 125
 Leu Glu Phe Thr Ser Arg Ser Gln Ser Thr Ser Ala Leu Leu Ser Ser
 130 135 140
 Lys Ser Thr Ser Ala Ser Pro Ala Asp Ala Ala Ala Cys Ala Ser
 145 150 155 160
 Pro Ser Ser Ser Ser Cys Lys Arg Ser Tyr Ser Ser Ala Gln Leu Glu
 165 170 175
 Thr Thr Gly Ser Asp Ala Pro Lys Lys Asp Lys Leu Gly Cys Thr Pro
 180 185 190
 Tyr Thr Arg Lys Gln Arg Asn Asn Pro Leu Pro Pro Val Ile Pro Lys
 195 200 205
 Gly Gln Asp Val Ala Ser Met Lys Arg Ala Arg Asn Thr Glu Ala Ala
 210 215 220
 Arg Arg Ser Arg Ala Arg Lys Met Glu Arg Met Ser Gln Leu Glu Glu
 225 230 235 240
 Lys Cys Gln Ser Leu Leu Lys Glu Asn Asp Asp Leu Lys Ala Gln Val
 245 250 255
 Gln Ala Leu Lys Lys Leu Leu Gly Gln Gln
 260 265

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ser Gln His Phe Thr Ser Ile Phe Glu Asn Leu Arg Phe Val Thr
 1 5 10 15
 Ile Lys Arg Ala Thr Asn Ala Gln Gln Gln Gln Gln Gln Gln Gln
 20 25 30
 Gln Gln Leu Gln Gln Gln Gln Gln Gln Leu Gln Gln Gln Lys Ala Gln
 35 40 45
 Thr Gln Gln Gln Asn Ser Arg Lys Ile Lys Thr Gln Ala Thr Pro Thr
 50 55 60
 Leu Asn Gly Asn Gly Leu Leu Ser Gly Asn Pro Asn Gly Gly Gly Gly
 65 70 75 80
 Asp Ser Ser Pro Ser His Glu Val Asp His Pro Gly Gly Ala Gln Gly
 85 90 95

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Ala Gln Ala Ala Gly Gly Leu Pro Ser Leu Ser Gly Thr Pro Leu Arg
 100 105 110
 His His Lys Arg Ala Ser Ile Ser Thr Ala Ser Pro Pro Ile Arg Glu
 115 120 125
 Arg Arg Gly Thr Asn Thr Ser Ile Val Val Glu Leu Asp Gly Ser Gly
 130 135 140
 Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Gly Val Gly Gln Gly Ala
 145 150 155 160
 Gly Cys Pro Pro Ser Gly Ser Cys Thr Ala Ser Gly Lys Ser Ser Arg
 165 170 175
 Glu Leu Ser Pro Ser Pro Lys Asn Gln Gln Gln Pro Arg Lys Met Ser
 180 185 190
 Gln Asp Tyr Arg Ser Arg Ala Gly Ser Phe Met His Leu Asp Asp Glu
 195 200 205
 Gly Arg Ser Leu Leu Met Arg Lys Pro Met Arg Leu Lys Asn Ile Glu
 210 215 220
 Gly Arg Pro Glu Val Tyr Asp Thr Leu His Cys Lys Gly Arg Glu Ile
 225 230 235 240
 Leu Ser Cys Ser Lys Ala Thr Cys Thr Ser Ser Ile Met Asn Ile Gly
 245 250 255
 Asn Ala Ala Val Glu Ala Arg Lys Ser Asp Leu Ile Leu Glu His Ala
 260 265 270
 Lys Asp Phe Leu Glu Gln Tyr Phe Thr Ser Ile Lys Arg Thr Ser Cys
 275 280 285
 Thr Ala His Glu Thr Arg Trp Lys Gln Val Arg Gln Ser Ile Glu Thr
 290 295 300
 Thr Gly His Tyr Gln Leu Thr Glu Thr Glu Leu Ile Tyr Gly Ala Lys
 305 310 315 320
 Leu Ala Trp Arg Asn Ser Ser Arg Cys Ile Gly Arg Ile Gln Trp Ser
 325 330 335
 Lys Leu Gln Val Phe Asp Cys Arg Tyr Val Thr Thr Thr Ser Gly Met
 340 345 350
 Phe Glu Ala Ile Cys Asn His Ile Lys Tyr Ala Thr Asn Lys Gly Asn
 355 360 365
 Leu Arg Ser Ala Ile Thr Ile Phe Pro Gln Arg Thr Asp Ala Lys His
 370 375 380
 Asp Tyr Arg Ile Trp Asn Asn Gln Leu Ile Ser Tyr Ala Gly Tyr Lys
 385 390 395 400
 Gln Ala Asp Gly Lys Ile Ile Gly Asp Pro Met Asn Val Glu Phe Thr
 405 410 415
 Glu Val Cys Thr Lys Leu Gly Trp Lys Ser Lys Gly Ser Glu Trp Asp
 420 425 430

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Ile Leu Pro Leu Val Val Ser Ala Asn Gly His Asp Pro Asp Tyr Phe
 435 440 445
 Asp Tyr Pro Pro Glu Leu Ile Leu Glu Val Pro Leu Thr His Pro Lys
 450 455 460
 Phe Glu Trp Phe Ser Asp Leu Gly Leu Arg Trp Tyr Ala Leu Pro Ala
 465 470 475 480
 Val Ser Ser Met Leu Phe Asp Val Gly Gly Ile Gln Phe Thr Ala Thr
 485 490 495
 Thr Phe Ser Gly Trp Tyr Met Ser Thr Glu Ile Gly Ser Arg Asn Leu
 500 505 510
 Cys Asp Thr Asn Arg Arg Asn Met Leu Glu Thr Val Ala Leu Lys Met
 515 520 525
 Gln Leu Asp Thr Arg Thr Pro Thr Ser Leu Trp Lys Asp Lys Ala Val
 530 535 540
 Val Glu Met Asn Ile Ala Val Leu His Ser Tyr Gln Ser Arg Asn Val
 545 550 555 560
 Thr Ile Val Asp His His Thr Ala Ser Glu Ser Phe Met Lys His Phe
 565 570 575
 Glu Asn Glu Ser Lys Leu Arg Asn Gly Cys Pro Ala Asp Trp Ile Trp
 580 585 590
 Ile Val Pro Pro Leu Ser Gly Ser Ile Thr Pro Val Phe His Gln Glu
 595 600 605
 Met Ala Leu Tyr Tyr Leu Lys Pro Ser Phe Glu Tyr Gln Asp Pro Ala
 610 615 620
 Trp Arg Thr His Val Trp Lys Lys Gly Arg Gly Glu Ser Lys Gly Lys
 625 630 635 640
 Lys Pro Arg Arg Lys Phe Asn Phe Lys Gln Ile Ala Arg Ala Val Lys
 645 650 655
 Phe Thr Ser Lys Leu Phe Gly Arg Ala Leu Ser Lys Arg Ile Lys Ala
 660 665 670
 Thr Val Leu Tyr Ala Thr Glu Thr Gly Lys Ser Glu Gln Tyr Ala Lys
 675 680 685
 Gln Leu Cys Glu Leu Leu Gly His Ala Phe Asn Ala Gln Ile Tyr Cys
 690 695 700
 Met Ser Asp Tyr Asp Ile Ser Ser Ile Glu His Glu Ala Leu Leu Ile
 705 710 715 720
 Val Val Ala Ser Thr Phe Gly Asn Gly Asp Pro Pro Glu Asn Gly Glu
 725 730 735
 Leu Phe Ser Gln Glu Leu Tyr Ala Met Arg Val Gln Glu Ser Ser Glu
 740 745 750
 His Gly Leu Gln Asp Ser Ser Ile Gly Ser Ser Lys Ser Phe Met Lys
 755 760 765

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Ala Ser Ser Arg Gln Glu Phe Met Lys Leu Pro Leu Gln Gln Val Lys
 770 775 780
 Arg Ile Asp Arg Trp Asp Ser Leu Arg Gly Ser Thr Ser Asp Thr Phe
 785 790 795 800
 Thr Glu Glu Thr Phe Gly Pro Leu Ser Asn Val Arg Phe Ala Val Phe
 805 810 815
 Ala Leu Gly Ser Ser Ala Tyr Pro Asn Phe Cys Ala Phe Gly Gln Tyr
 820 825 830
 Val Asp Asn Ile Leu Gly Glu Leu Gly Gly Glu Arg Leu Leu Arg Val
 835 840 845
 Ala Tyr Gly Asp Glu Met Cys Gly Gln Glu Gln Ser Phe Arg Lys Trp
 850 855 860
 Ala Pro Glu Val Phe Lys Leu Ala Cys Glu Thr Phe Cys Leu Asp Pro
 865 870 875 880
 Glu Glu Ser Leu Ser Asp Ala Ser Leu Ala Leu Gln Asn Asp Ser Leu
 885 890 895
 Thr Val Asn Thr Val Arg Leu Val Pro Ser Ala Asn Lys Gly Ser Leu
 900 905 910
 Asp Ser Ser Leu Ser Lys Tyr His Asn Lys Lys Val His Cys Cys Lys
 915 920 925
 Ala Lys Ala Lys Pro His Asn Leu Thr Arg Leu Ser Glu Gly Ala Lys
 930 935 940
 Thr Thr Met Leu Leu Glu Ile Cys Ala Pro Gly Leu Glu Tyr Glu Pro
 945 950 955 960
 Gly Asp His Val Gly Ile Phe Pro Ala Asn Arg Thr Glu Leu Val Asp
 965 970 975
 Gly Leu Leu Asn Arg Leu Val Gly Val Asp Asn Pro Asp Glu Val Leu
 980 985 990
 Gln Leu Gln Leu Leu Lys Glu Lys Gln Thr Ser Asn Gly Ile Phe Lys
 995 1000 1005
 Cys Trp Glu Pro His Asp Lys Ile Pro Pro Asp Thr Leu Arg Asn Leu
 1010 1015 1020
 Leu Ala Arg Phe Phe Asp Leu Thr Thr Pro Pro Ser Arg Gln Leu Leu
 1025 1030 1035 1040
 Thr Leu Leu Ala Gly Phe Cys Glu Asp Thr Ala Asp Lys Glu Arg Leu
 1045 1050 1055
 Glu Leu Leu Val Asn Asp Ser Ser Ala Tyr Glu Asp Trp Arg His Trp
 1060 1065 1070
 Arg Leu Pro His Leu Leu Asp Val Leu Glu Glu Phe Pro Ser Cys Arg
 1075 1080 1085
 Pro Pro Ala Pro Leu Leu Leu Ala Gln Leu Thr Pro Leu Gln Pro Arg
 1090 1095 1100

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Phe Tyr Ser Ile Ser Ser Ser Pro Arg Arg Val Ser Asp Glu Ile His
 1105 1110 1115 1120
 Leu Thr Val Ala Ile Val Lys Tyr Arg Cys Glu Asp Gly Gln Gly Asp
 1125 1130 1135
 Glu Arg Tyr Gly Val Cys Ser Asn Tyr Leu Ser Gly Leu Arg Ala Asp
 1140 1145 1150
 Asp Glu Leu Phe Met Phe Val Arg Ser Ala Leu Gly Phe His Leu Pro
 1155 1160 1165
 Ser Asp Arg Ser Arg Pro Ile Ile Leu Ile Gly Pro Gly Thr Gly Ile
 1170 1175 1180
 Ala Pro Phe Arg Ser Phe Trp Gln Glu Phe Gln Val Leu Arg Asp Leu
 1185 1190 1195 1200
 Asp Pro Thr Ala Lys Leu Pro Lys Met Trp Leu Phe Phe Gly Cys Arg
 1205 1210 1215
 Asn Arg Asp Val Asp Leu Tyr Ala Glu Glu Lys Ala Glu Leu Gln Lys
 1220 1225 1230
 Asp Gln Ile Leu Asp Arg Val Phe Leu Ala Leu Ser Arg Glu Gln Ala
 1235 1240 1245
 Ile Pro Lys Thr Tyr Val Gln Asp Leu Ile Glu Gln Glu Phe Asp Ser
 1250 1255 1260
 Leu Tyr Gln Leu Ile Val Gln Glu Arg Gly His Ile Tyr Val Cys Gly
 1265 1270 1275 1280
 Asp Val Thr Met Ala Glu His Val Tyr Gln Thr Ile Arg Lys Cys Ile
 1285 1290 1295
 Ala Gly Lys Glu Gln Lys Ser Glu Ala Glu Val Glu Thr Phe Leu Leu
 1300 1305 1310
 Thr Leu Arg Asp Glu Ser Arg Tyr His Glu Asp Ile Phe Gly Ile Thr
 1315 1320 1325
 Leu Arg Thr Ala Glu Ile His Thr Lys Ser Arg Ala Thr Ala Arg Ile
 1330 1335 1340
 Arg Met Ala Ser Gln Pro
 1345 1350

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Asn Leu Lys Ser Val Gly Gln Glu Pro Gly Pro Pro Cys Gly
 1 5 10 15
 Leu Gly Leu Gly Leu Gly Leu Gly Leu Cys Gly Lys Gln Gly Pro Ala
 20 25 30
 Ser Pro Ala Pro Glu Pro Ser Arg Ala Pro Ala Pro Ala Thr Pro His
 35 40 45
 Ala Pro Asp His Ser Pro Ala Pro Asn Ser Pro Thr Leu Thr Arg Pro
 50 55 60
 Pro Glu Gly Pro Lys Phe Pro Arg Val Lys Asn Trp Glu Leu Gly Ser
 65 70 75 80
 Ile Thr Tyr Asp Thr Leu Cys Ala Gln Ser Gln Gln Asp Gly Pro Cys
 85 90 95
 Thr Pro Arg Arg Cys Leu Gly Ser Leu Val Leu Pro Arg Lys Leu Gln
 100 105 110
 Thr Arg Pro Ser Pro Gly Pro Pro Pro Ala Glu Gln Leu Leu Ser Gln
 115 120 125
 Ala Arg Asp Phe Ile Asn Gln Tyr Tyr Ser Ser Ile Lys Arg Ser Gly
 130 135 140
 Ser Gln Ala His Glu Glu Arg Leu Gln Glu Val Glu Ala Glu Val Ala
 145 150 155 160
 Ser Thr Gly Thr Ile His Leu Arg Glu Ser Glu Leu Val Phe Gly Ala
 165 170 175
 Lys Gln Ala Trp Arg Asn Ala Pro Arg Cys Val Gly Arg Ile Gln Trp
 180 185 190
 Gly Lys Leu Gln Val Phe Asp Ala Arg Asp Cys Ser Ser Ala Gln Glu
 195 200 205
 Met Phe Thr Tyr Ile Cys Asn His Ile Lys Tyr Ala Thr Asn Arg Gly
 210 215 220
 Asn Leu Arg Ser Ala Ile Thr Val Phe Pro Gln Arg Ala Pro Gly Arg
 225 230 235 240
 Gly Asp Phe Arg Ile Trp Asn Ser Gln Leu Val Arg Tyr Ala Gly Tyr
 245 250 255
 Arg Gln Gln Asp Gly Ser Val Arg Gly Asp Pro Ala Asn Val Glu Ile
 260 265 270
 Thr Glu Leu Cys Ile Gln His Gly Trp Thr Pro Gly Asn Gly Arg Phe
 275 280 285
 Asp Val Leu Pro Leu Leu Leu Gln Ala Pro Asp Glu Ala Pro Glu Leu
 290 295 300
 Phe Val Leu Pro Pro Glu Leu Val Leu Glu Val Pro Leu Gly Ala Pro
 305 310 315 320

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His Thr Gly Val Val Arg Gly Pro Gly Leu Arg Trp Tyr Ala Leu Pro
 325 330 335
 Ala Val Ser Asn Met Leu Leu Glu Ile Gly Gly Leu Glu Phe Ser Ala
 340 345 350
 Ala Pro Phe Ser Gly Trp Tyr Met Ser Thr Glu Ile Gly Thr Arg Asn
 355 360 365
 Leu Cys Asp Pro His Arg Tyr Asn Ile Leu Glu Asp Val Ala Val Cys
 370 375 380
 Met Asp Leu Asp Thr Arg Thr Thr Ser Ser Leu Trp Lys Asp Lys Ala
 385 390 395 400
 Ala Val Glu Ile Asn Leu Ala Val Leu His Ser Phe Gln Leu Ala Lys
 405 410 415
 Val Thr Ile Val Asp His His Ala Ala Thr Val Ser Phe Met Lys His
 420 425 430
 Leu Asp Asn Glu Gln Lys Ala Arg Gly Gly Cys Pro Ala Asp Trp Ala
 435 440 445
 Trp Ile Val Pro Pro Ile Tyr Gly Ser Leu Pro Pro Val Phe His Gln
 450 455 460
 Glu Met Val Asn Tyr Ile Leu Ser Pro Ala Phe Arg Tyr Gln Pro Asp
 465 470 475 480
 Pro Trp Lys Gly Ser Ala Thr Lys Gly Ala Gly Ile Thr Arg Lys Lys
 485 490 495
 Thr Phe Lys Glu Val Ala Asn Ala Val Lys Ile Ser Ala Ser Leu Met
 500 505 510
 Gly Thr Leu Met Ala Lys Arg Val Lys Ala Thr Ile Leu Tyr Ala Ser
 515 520 525
 Glu Thr Gly Arg Ala Gln Ser Tyr Ala Gln Gln Leu Gly Arg Leu Phe
 530 535 540
 Arg Lys Ala Phe Asp Pro Arg Val Leu Cys Met Asp Glu Tyr Asp Val
 545 550 555 560
 Val Ser Leu Glu His Glu Ala Leu Val Leu Val Val Thr Ser Thr Phe
 565 570 575
 Gly Asn Gly Asp Pro Pro Glu Asn Gly Glu Ser Phe Ala Ala Ala Leu
 580 585 590
 Met Glu Met Ser Gly Pro Tyr Asn Ser Ser Pro Arg Pro Glu Gln His
 595 600 605
 Lys Ser Tyr Lys Ile Arg Phe Asn Ser Val Ser Cys Ser Asp Pro Leu
 610 615 620
 Val Ser Ser Trp Arg Arg Lys Arg Lys Glu Ser Ser Asn Thr Asp Ser
 625 630 635 640
 Ala Gly Ala Leu Gly Thr Leu Arg Phe Cys Val Phe Gly Leu Gly Ser
 645 650 655

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Arg Ala Tyr Pro His Phe Cys Ala Phe Ala Arg Ala Val Asp Thr Arg
 660 665 670
 Leu Glu Glu Leu Gly Gly Glu Arg Leu Leu Gln Leu Gly Gln Gly Asp
 675 680 685
 Glu Leu Cys Gly Gln Glu Glu Ala Phe Arg Gly Trp Ala Lys Ala Ala
 690 695 700
 Phe Gln Ala Ser Cys Glu Thr Phe Cys Val Gly Glu Glu Ala Lys Ala
 705 710 715 720
 Ala Ala Gln Asp Ile Phe Ser Pro Lys Arg Ser Trp Lys Arg Gln Arg
 725 730 735
 Tyr Arg Leu Ser Ala Gln Ala Glu Gly Leu Gln Leu Leu Pro Gly Leu
 740 745 750
 Ile His Val His Arg Arg Lys Met Phe Gln Ala Thr Val Leu Ser Val
 755 760 765
 Glu Asn Leu Gln Ser Ser Lys Ser Thr Arg Ala Thr Ile Leu Val Arg
 770 775 780
 Leu Asp Thr Ala Gly Gln Glu Gly Leu Gln Tyr Gln Pro Gly Asp His
 785 790 795 800
 Ile Gly Ile Ser Ala Pro Asn Arg Pro Gly Leu Val Glu Ala Leu Leu
 805 810 815
 Ser Arg Val Glu Asp Pro Pro Pro Pro Thr Glu Ser Val Ala Val Glu
 820 825 830
 Gln Leu Glu Lys Gly Ser Pro Gly Gly Pro Pro Pro Ser Trp Val Arg
 835 840 845
 Asp Pro Arg Leu Pro Pro Cys Thr Val Arg Gln Ala Leu Thr Phe Phe
 850 855 860
 Leu Asp Ile Thr Ser Pro Pro Ser Pro Arg Leu Leu Arg Leu Leu Ser
 865 870 875 880
 Thr Leu Ala Glu Glu Pro Ser Glu Gln Gln Glu Leu Glu Thr Leu Ser
 885 890 895
 Gln Asp Pro Arg Arg Tyr Glu Glu Trp Lys Leu Val Arg Cys Pro Thr
 900 905 910
 Leu Leu Glu Val Leu Glu Gln Phe Pro Ser Val Ala Leu Pro Ala Pro
 915 920 925
 Leu Leu Leu Thr Gln Leu Pro Leu Leu Gln Pro Arg Tyr Tyr Ser Val
 930 935 940
 Ser Ser Ala Pro Asn Ala His Pro Gly Glu Val His Leu Thr Val Ala
 945 950 955 960
 Val Leu Ala Tyr Arg Thr Gln Asp Gly Leu Gly Pro Leu His Tyr Gly
 965 970 975
 Val Cys Ser Thr Trp Leu Ser Gln Leu Lys Thr Gly Asp Pro Val Pro
 980 985 990

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Cys Phe Ile Arg Gly Ala Pro Ser Phe Arg Leu Pro Pro Asp Pro Tyr
 995 1000 1005
 Val Pro Cys Ile Leu Val Gly Pro Gly Thr Gly Ile Ala Pro Phe Arg
 1010 1015 1020
 Gly Phe Trp Gln Glu Arg Leu His Asp Ile Glu Ser Lys Gly Leu Gln
 1025 1030 1035 1040
 Pro His Pro Met Thr Leu Val Phe Gly Cys Arg Cys Ser Gln Leu Asp
 1045 1050 1055
 His Leu Tyr Arg Asp Glu Val Gln Asp Ala Gln Glu Arg Gly Val Phe
 1060 1065 1070
 Gly Arg Val Leu Thr Ala Phe Ser Arg Glu Pro Asp Ser Pro Lys Thr
 1075 1080 1085
 Tyr Val Gln Asp Ile Leu Arg Thr Glu Leu Ala Ala Glu Val His Arg
 1090 1095 1100
 Val Leu Cys Leu Glu Arg Gly His Met Phe Val Cys Gly Asp Val Thr
 1105 1110 1115 1120
 Met Ala Thr Ser Val Leu Gln Thr Val Gln Arg Ile Leu Ala Thr Glu
 1125 1130 1135
 Gly Asp Met Glu Leu Asp Glu Ala Gly Asp Val Ile Gly Val Leu Arg
 1140 1145 1150
 Asp Gln Gln Arg Tyr His Glu Asp Ile Phe Gly Leu Thr Leu Arg Thr
 1155 1160 1165
 Gln Glu Val Thr Ser Arg Ile Arg Thr Gln Ser Phe Ser Leu Gln Glu
 1170 1175 1180
 Arg His Leu Arg Gly Ala Val Pro Trp Ala Phe Asp Pro Pro Gly Pro
 1185 1190 1195 1200
 Asp Thr Pro Gly Pro
 1205

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Glu Asn Thr Phe Gly Val Gln Gln Ile Gln Pro Asn Val Ile
 1 5 10 15
 Ser Val Arg Leu Phe Lys Arg Lys Val Gly Gly Leu Gly Phe Leu Val
 20 25 30

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Lys Glu Arg Val Ser Lys Pro Pro Val Ile Ile Ser Asp Leu Ile Arg
 35 40 45
 Gly Gly Ala Ala Glu Gln Ser Gly Leu Ile Gln Ala Gly Asp Ile Ile
 50 55 60
 Leu Ala Val Asn Asp Arg Pro Leu Val Asp Leu Ser Tyr Asp Ser Ala
 65 70 75 80
 Leu Glu Val Leu Arg Gly Ile Ala Ser Glu Thr His Val Val Leu Ile
 85 90 95
 Leu Arg Gly Pro Glu Gly Phe Thr Thr His Leu Glu Thr Thr Phe Thr
 100 105 110
 Gly Asp Gly Thr Pro Lys Thr Ile Arg Val Thr Gln Pro Leu Gly Pro
 115 120 125
 Pro Thr Lys Ala Val Asp Leu Ser His Gln Pro Ser Ala Ser Lys Asp
 130 135 140
 Gln Ser Leu Ala Val Asp Arg Val Thr Gly Leu Gly Asn Gly Pro Gln
 145 150 155 160
 His Ala Gln Gly His Gly Gln Gly Ala Gly Ser Val Ser Gln Ala Asn
 165 170 175
 Gly Val Ala Ile Asp Pro Thr Met Lys Ser Thr Lys Ala Asn Leu Gln
 180 185 190
 Asp Ile Gly Glu His Asp Glu Leu Leu Lys Glu Ile Glu Pro Val Leu
 195 200 205
 Ser Ile Leu Asn Ser Gly Ser Lys Ala Thr Asn Arg Gly Gly Pro Ala
 210 215 220
 Lys Ala Glu Met Lys Asp Thr Gly Ile Gln Val Asp Arg Asp Leu Asp
 225 230 235 240
 Gly Lys Ser His Lys Ala Pro Pro Leu Gly Gly Asp Asn Asp Arg Val
 245 250 255
 Phe Asn Asp Leu Trp Gly Lys Asp Asn Val Pro Val Ile Leu Asn Asn
 260 265 270
 Pro Tyr Ser Glu Lys Glu Gln Ser Pro Thr Ser Gly Lys Gln Ser Pro
 275 280 285
 Thr Lys Asn Gly Ser Pro Ser Arg Cys Pro Arg Phe Leu Lys Val Lys
 290 295 300
 Asn Trp Glu Thr Asp Val Val Leu Thr Asp Thr Leu His Leu Lys Ser
 305 310 315 320
 Thr Leu Glu Thr Gly Cys Thr Glu His Ile Cys Met Gly Ser Ile Met
 325 330 335
 Leu Pro Ser Gln His Thr Arg Lys Pro Glu Asp Val Arg Thr Lys Asp
 340 345 350
 Gln Leu Phe Pro Leu Ala Lys Glu Phe Leu Asp Gln Tyr Tyr Ser Ser
 355 360 365

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Ile Lys Arg Phe Gly Ser Lys Ala His Met Asp Arg Leu Glu Glu Val
 370 375 380
 Asn Lys Glu Ile Glu Ser Thr Ser Thr Tyr Gln Leu Lys Asp Thr Glu
 385 390 395 400
 Leu Ile Tyr Gly Ala Lys His Ala Trp Arg Asn Ala Ser Arg Cys Val
 405 410 415
 Gly Arg Ile Gln Trp Ser Lys Leu Gln Val Phe Asp Ala Arg Asp Cys
 420 425 430
 Thr Thr Ala His Gly Met Phe Asn Tyr Ile Cys Asn His Val Lys Tyr
 435 440 445
 Ala Thr Asn Lys Gly Asn Leu Arg Ser Ala Ile Thr Ile Phe Pro Gln
 450 455 460
 Arg Thr Asp Gly Lys His Asp Phe Arg Val Trp Asn Ser Gln Leu Ile
 465 470 475 480
 Arg Tyr Ala Gly Tyr Lys Gln Pro Asp Gly Ser Thr Leu Gly Asp Pro
 485 490 495
 Ala Asn Val Gln Phe Thr Glu Ile Cys Ile Gln Gln Gly Trp Lys Ala
 500 505 510
 Pro Arg Gly Arg Phe Asp Val Leu Pro Leu Leu Leu Gln Ala Asn Gly
 515 520 525
 Asn Asp Pro Glu Leu Phe Gln Ile Pro Pro Glu Leu Val Leu Glu Val
 530 535 540
 Pro Ile Arg His Pro Lys Phe Asp Trp Phe Lys Asp Leu Gly Leu Lys
 545 550 555 560
 Trp Tyr Gly Leu Pro Ala Val Ser Asn Met Leu Leu Glu Ile Gly Gly
 565 570 575
 Leu Glu Phe Ser Ala Cys Pro Phe Ser Gly Trp Tyr Met Gly Thr Glu
 580 585 590
 Ile Gly Val Arg Asp Tyr Cys Asp Asn Ser Arg Tyr Asn Ile Leu Glu
 595 600 605
 Glu Val Ala Lys Lys Met Asp Leu Asp Met Arg Lys Thr Ser Ser Leu
 610 615 620
 Trp Lys Asp Gln Ala Leu Val Glu Ile Asn Ile Ala Val Leu Tyr Ser
 625 630 635 640
 Phe Gln Ser Asp Lys Val Thr Ile Val Asp His His Ser Ala Thr Glu
 645 650 655
 Ser Phe Ile Lys His Met Glu Asn Glu Tyr Arg Cys Arg Gly Gly Cys
 660 665 670
 Pro Ala Asp Trp Val Trp Ile Val Pro Pro Met Ser Gly Ser Ile Thr
 675 680 685
 Pro Val Phe His Gln Glu Met Leu Asn Tyr Arg Leu Thr Pro Ser Phe
 690 695 700

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Glu Tyr Gln Pro Asp Pro Trp Asn Thr His Val Trp Lys Gly Thr Asn
 705 710 715 720
 Gly Thr Pro Thr Lys Arg Arg Ala Ile Gly Phe Lys Lys Leu Ala Glu
 725 730 735
 Ala Val Lys Phe Ser Ala Lys Leu Met Gly Gln Ala Met Ala Lys Arg
 740 745 750
 Val Lys Ala Thr Ile Leu Tyr Ala Thr Glu Thr Gly Lys Ser Gln Ala
 755 760 765
 Tyr Ala Lys Thr Leu Cys Glu Ile Phe Lys His Ala Phe Asp Ala Lys
 770 775 780
 Ala Met Ser Met Glu Glu Tyr Asp Ile Val His Leu Glu His Glu Ala
 785 790 795 800
 Leu Val Leu Val Val Thr Ser Thr Phe Gly Asn Gly Asp Pro Pro Glu
 805 810 815
 Asn Gly Glu Lys Phe Gly Cys Ala Leu Met Glu Met Arg His Pro Asn
 820 825 830
 Ser Val Gln Glu Glu Arg Lys Ser Tyr Lys Val Arg Phe Asn Ser Val
 835 840 845
 Ser Ser Tyr Ser Asp Ser Arg Lys Ser Ser Gly Asp Gly Pro Asp Leu
 850 855 860
 Arg Asp Asn Phe Glu Ser Thr Gly Pro Leu Ala Asn Val Arg Phe Ser
 865 870 875 880
 Val Phe Gly Leu Gly Ser Arg Ala Tyr Pro His Phe Cys Ala Phe Gly
 885 890 895
 His Ala Val Asp Thr Leu Leu Glu Glu Leu Gly Gly Glu Arg Ile Leu
 900 905 910
 Lys Met Arg Glu Gly Asp Glu Leu Cys Gly Gln Glu Glu Ala Phe Arg
 915 920 925
 Thr Trp Ala Lys Lys Val Phe Lys Ala Ala Cys Asp Val Phe Cys Val
 930 935 940
 Gly Asp Asp Val Asn Ile Glu Lys Pro Asn Asn Ser Leu Ile Ser Asn
 945 950 955 960
 Asp Arg Ser Trp Lys Arg Asn Lys Phe Arg Leu Thr Tyr Val Ala Glu
 965 970 975
 Ala Pro Asp Leu Thr Gln Gly Leu Ser Asn Val His Lys Lys Arg Val
 980 985 990
 Ser Ala Ala Arg Leu Leu Ser Arg Gln Asn Leu Gln Ser Pro Lys Phe
 995 1000 1005
 Ser Arg Ser Thr Ile Phe Val Arg Leu His Thr Asn Gly Asn Gln Glu
 1010 1015 1020
 Leu Gln Tyr Gln Pro Gly Asp His Leu Gly Val Phe Pro Gly Asn His
 1025 1030 1035 1040

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Glu Asp Leu Val Asn Ala Leu Ile Glu Arg Leu Glu Asp Ala Pro Pro
 1045 1050 1055
 Ala Asn His Val Val Lys Val Glu Met Leu Glu Glu Arg Asn Thr Ala
 1060 1065 1070
 Leu Gly Val Ile Ser Asn Trp Lys Asp Glu Ser Arg Leu Pro Pro Cys
 1075 1080 1085
 Thr Ile Phe Gln Ala Phe Lys Tyr Tyr Leu Asp Ile Thr Thr Pro Pro
 1090 1095 1100
 Thr Pro Leu Gln Leu Gln Gln Phe Ala Ser Leu Ala Thr Asn Glu Lys
 1105 1110 1115 1120
 Glu Lys Gln Arg Leu Leu Val Leu Ser Lys Gly Leu Gln Glu Tyr Glu
 1125 1130 1135
 Glu Trp Lys Trp Gly Lys Asn Pro Thr Met Val Glu Val Leu Glu Glu
 1140 1145 1150
 Phe Pro Ser Ile Gln Met Pro Ala Thr Leu Leu Leu Thr Gln Leu Ser
 1155 1160 1165
 Leu Leu Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Asp Met Tyr
 1170 1175 1180
 Pro Asp Glu Val His Leu Thr Val Ala Ile Val Ser Tyr His Thr Arg
 1185 1190 1195 1200
 Asp Gly Glu Gly Pro Val His His Gly Val Cys Ser Ser Trp Leu Asn
 1205 1210 1215
 Arg Ile Gln Ala Asp Asp Val Val Pro Cys Phe Val Arg Gly Ala Pro
 1220 1225 1230
 Ser Phe His Leu Pro Arg Asn Pro Gln Val Pro Cys Ile Leu Val Gly
 1235 1240 1245
 Pro Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe Trp Gln Gln Arg Gln
 1250 1255 1260
 Phe Asp Ile Gln His Lys Gly Met Asn Pro Cys Pro Met Val Leu Val
 1265 1270 1275 1280
 Phe Gly Cys Arg Gln Ser Lys Ile Asp His Ile Tyr Arg Glu Glu Thr
 1285 1290 1295
 Leu Gln Ala Lys Asn Lys Gly Val Phe Arg Glu Leu Tyr Thr Ala Tyr
 1300 1305 1310
 Ser Arg Glu Pro Asp Arg Pro Lys Lys Tyr Val Gln Asp Val Leu Gln
 1315 1320 1325
 Glu Gln Leu Ala Glu Ser Val Tyr Arg Ala Leu Lys Glu Gln Gly Gly
 1330 1335 1340
 His Ile Tyr Val Cys Gly Asp Val Thr Met Ala Ala Asp Val Leu Lys
 1345 1350 1355 1360
 Ala Ile Gln Arg Ile Met Thr Gln Gln Gly Lys Leu Ser Glu Glu Asp
 1365 1370 1375

Ala Gly Val Phe Ile Ser Arg Leu Arg Asp Asp Asn Arg Tyr His Glu
1380 1385 1390

Asp Ile Phe Gly Val Thr Leu Arg Thr Tyr Glu Val Thr Asn Arg Leu
1395 1400 1405

Arg Ser Glu Ser Ile Ala Phe Ile Glu Glu Ser Lys Lys Asp Ala Asp
1410 1415 1420

Glu Val Phe Ser Ser
1425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

BNSDOCID: <WO_____9611270A1 IA>

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Arg Cys Ile Gly Arg Ile Gln Trp Ser Asn Leu Gln Val Phe Asp Ala
 195 200 205
 Arg Asn Cys Ser Thr Ala Gln Glu Met Phe Gln His Ile Cys Arg His
 210 215 220
 Ile Leu Tyr Ala Thr Asn Asn Gly Asn Ile Arg Ser Ala Ile Thr Val
 225 230 235 240
 Phe Pro Gln Arg Ser Asp Gly Lys His Asp Phe Arg Leu Trp Asn Ser
 245 250 255
 Gln Leu Ile Arg Tyr Ala Gly Tyr Gln Met Pro Asp Gly Thr Ile Arg
 260 265 270
 Gly Asp Ala Ala Thr Leu Glu Phe Thr Gln Leu Cys Ile Asp Leu Gly
 275 280 285
 Trp Lys Pro Arg Tyr Gly Arg Phe Asp Val Leu Pro Leu Val Leu Gln
 290 295 300
 Ala Asp Gly Gln Asp Pro Glu Val Phe Glu Ile Pro Pro Asp Leu Val
 305 310 315 320
 Leu Glu Val Thr Met Glu His Pro Lys Tyr Glu Trp Phe Gln Glu Leu
 325 330 335
 Gly Leu Lys Trp Tyr Ala Leu Pro Ala Val Ala Asn Met Leu Leu Glu
 340 345 350
 Val Gly Gly Leu Glu Phe Pro Ala Cys Pro Phe Asn Gly Trp Tyr Met
 355 360 365
 Gly Thr Glu Ile Gly Val Arg Asp Phe Cys Asp Thr Gln Arg Tyr Asn
 370 375 380
 Ile Leu Glu Glu Val Gly Arg Arg Met Gly Leu Glu Thr His Thr Leu
 385 390 395 400
 Ala Ser Leu Trp Lys Asp Arg Ala Val Thr Glu Ile Asn Val Ala Val
 405 410 415
 Leu His Ser Phe Gln Lys Gln Asn Val Thr Ile Met Asp His His Thr
 420 425 430
 Ala Ser Glu Ser Phe Met Lys His Met Gln Asn Glu Tyr Arg Ala Arg
 435 440 445
 Gly Gly Cys Pro Ala Asp Trp Ile Trp Leu Val Pro Pro Val Ser Gly
 450 455 460
 Ser Ile Thr Pro Val Phe His Gln Glu Met Leu Asn Tyr Val Leu Ser
 465 470 475 480
 Pro Phe Tyr Tyr Tyr Gln Ile Glu Pro Trp Lys Thr His Ile Trp Gln
 485 490 495
 Asn Glu Lys Leu Arg Pro Arg Arg Arg Glu Ile Arg Phe Arg Val Leu
 500 505 510
 Val Lys Val Val Phe Phe Ala Ser Met Leu Met Arg Lys Val Met Ala
 515 520 525

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Ser Arg Val Arg Ala Thr Val Leu Phe Ala Thr Glu Thr Gly Lys Ser
 530 535 540
 Glu Ala Leu Ala Arg Asp Leu Ala Thr Leu Phe Ser Tyr Ala Phe Asn
 545 550 555 560
 Thr Lys Val Val Cys Met Asp Gln Tyr Lys Ala Ser Thr Leu Glu Glu
 565 570 575
 Glu Gln Leu Leu Leu Val Val Thr Ser Thr Phe Gly Asn Gly Asp Cys
 580 585 590
 Pro Ser Asn Gly Gln Thr Leu Lys Lys Ser Leu Phe Met Leu Arg Glu
 595 600 605
 Leu Asn His Thr Phe Arg Tyr Ala Val Phe Gly Leu Gly Ser Ser Met
 610 615 620
 Tyr Pro Gln Phe Cys Ala Phe Ala His Asp Ile Asp Gln Lys Leu Ser
 625 630 635 640
 His Leu Gly Ala Ser Gln Leu Ala Pro Thr Gly Glu Gly Asp Glu Leu
 645 650 655
 Ser Gly Gln Glu Asp Ala Phe Arg Ser Trp Ala Val Gln Thr Phe Arg
 660 665 670
 Ala Ala Cys Glu Thr Phe Asp Val Arg Ser Lys His His Ile Gln Ile
 675 680 685
 Pro Lys Arg Phe Thr Ser Asn Ala Thr Trp Glu Pro Gln Gln Tyr Arg
 690 695 700
 Leu Ile Gln Ser Pro Glu Pro Leu Asp Leu Asn Arg Ala Leu Ser Ser
 705 710 715 720
 Ile His Ala Lys Asn Val Phe Thr Met Arg Leu Lys Ser Gln Gln Asn
 725 730 735
 Leu Gln Ser Glu Lys Ser Ser Arg Thr Thr Leu Leu Val Gln Leu Thr
 740 745 750
 Phe Glu Gly Ser Arg Gly Pro Ser Tyr Leu Pro Gly Glu His Leu Gly
 755 760 765
 Ile Phe Pro Gly Asn Gln Thr Ala Leu Val Gln Gly Ile Leu Glu Arg
 770 775 780
 Val Val Asp Cys Pro Thr Pro His Gln Thr Val Cys Leu Glu Val Leu
 785 790 795 800
 Asp Glu Ser Gly Ser Tyr Trp Val Lys Asp Lys Arg Leu Pro Pro Cys
 805 810 815
 Ser Leu Ser Gln Ala Leu Thr Tyr Phe Leu Asp Ile Thr Thr Pro Pro
 820 825 830
 Thr Gln Leu Gln Leu His Lys Leu Ala Arg Phe Ala Thr Asp Glu Thr
 835 840 845
 Asp Arg Gln Arg Leu Glu Ala Leu Cys Gln Pro Ser Glu Tyr Asn Asp
 850 855 860

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Trp Lys Phe Ser Asn Asn Pro Thr Phe Leu Glu Val Leu Glu Glu Phe
 865 870 875 880
 Pro Ser Leu His Val Pro Ala Ala Phe Leu Leu Ser Gln Leu Pro Ile
 885 890 895
 Leu Lys Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Gln Asp His Thr Pro
 900 905 910
 Ser Glu Val His Leu Thr Val Ala Val Val Thr Tyr Arg Thr Arg Asp
 915 920 925
 Gly Gln Gly Pro Leu His His Gly Val Cys Ser Thr Trp Ile Arg Asn
 930 935 940
 Leu Lys Pro Gln Asp Pro Val Pro Cys Phe Val Arg Ser Val Ser Gly
 945 950 955 960
 Phe Gln Leu Pro Glu Asp Pro Ser Gln Pro Cys Ile Leu Ile Gly Pro
 965 970 975
 Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe Trp Gln Gln Arg Leu His
 980 985 990
 Asp Ser Gln His Lys Gly Leu Lys Gly Gly Arg Met Ser Leu Val Phe
 995 1000 1005
 Gly Cys Arg His Pro Glu Glu Asp His Leu Tyr Gln Glu Glu Met Gln
 1010 1015 1020
 Glu Met Val Arg Lys Arg Val Leu Phe Gln Val His Thr Gly Tyr Ser
 1025 1030 1035 1040
 Arg Leu Pro Gly Lys Pro Lys Val Tyr Val Gln Asp Ile Leu Gln Lys
 1045 1050 1055
 Gln Leu Ala Asn Glu Val Leu Ser Val Leu His Gly Glu Gln Gly His
 1060 1065 1070
 Leu Tyr Ile Cys Gly Asp Val Arg Met Ala Arg Asp Val Ala Thr Thr
 1075 1080 1085
 Leu Lys Lys Leu Val Ala Thr Lys Leu Asn Leu Ser Glu Glu Gln Val
 1090 1095 1100
 Glu Asp Tyr Phe Phe Gln Leu Lys Ser Gln Lys Arg Tyr His Glu Asp
 1105 1110 1115 1120
 Ile Phe Gly Ala Val Phe Ser Tyr Gly Ala Lys Lys Gly Ser Ala Leu
 1125 1130 1135
 Glu Glu Pro Lys Ala Thr Arg Leu
 1140

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Asp Pro Ala Asn Val Glu Phe Thr Glu Ile Cys Ile Gln Gln Gly
1 5 10 15
Trp Lys Pro Arg
 20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Asp Pro Met Asn Val Glu Phe Thr Glu Thr Val Ala Leu Lys Met
1 5 10 15
Gln Leu Asp Thr
 20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Asp Asn Ser Arg Tyr Asn Ile Leu Glu Glu Val Ala Lys Lys Met
1 5 10 15
Asp Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly Asp Pro Ala Asn Val Glu Phe Thr Glu Glu Val Ala Lys Lys Met
1 5 10 15
Asp Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGTCTAGATC TATGACTGAA TATGACGTAA TATGACGTAA TGGTACCAGA TCTGGCC

57

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAATGACGTA ACGGAAATGA CGTAACGGAA ATGACGTAAC G

41

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAATGAATTA ACGGAAATGA ATTAACGGAA ATGAATTAAC GG

42

(2) INFORMATION FOR SEQ ID NO:20:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGCACGGGTT TTCGACGTTT ACTGGTAGTG TCTGATGAGG CCGAAAGGCC GAAACGCGAT 60
GCCATAACC ACCACGCTCA G 81

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCGACCCACA GTTTCGGGTT TTCGAGCAAG TCTGCTAGTG TCTGATGAGG CCGAAAGGCC 60
GAAACGCGAA GCCGTATTGC ACCACGCTCA TCGAGAAGGC 100

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTAGAGCTTG CAAGCATGCT TGCAAGCAAG CATGCTTGCA AGCATGCTTG CAAGC 55

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCTAGAGCG TACGCAAGCG TACGCAAGCG TACG 34

(2) INFORMATION FOR SEQ ID NO:24:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Arg Lys Arg Glu Ile Arg Leu Gln Lys Asn Arg Glu Ala Ala Arg Glu
1 5 10 15

Cys

(A) LENGTH: 4491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

GAATTCGGTT	TTTGAAGAGT	GAAGCAATTG	AGTGCGGCC	GAAAAAGAGA	GCCGCAGAAA	60
GTTTGCGAAC	AGAATTTAAT	CAAAAACCTG	GAGGGTAAAT	TGTCCAAGTG	GTTCACCTGT	120
TGGCTGCATT	TTAAATCAAC	GAGGCAAACA	ATCAGCGCAG	AGGAGCTGCT	CCACGTTCCC	180
CGGACAAGAT	GTCGCAGCAT	TTCACATCGA	TATTTGAGAA	CCTGCGATTG	GTGACCATCA	240
AACGTGCGAC	AAATGCGCAA	CAGCAACAGC	AGCAGCAGCA	GCAACAGCAA	CTTCAGCAGC	300
AGCAGCAGCA	GCTGCAGCAA	CAGAAGGCAC	AGACACAGCA	ACAAAATAGC	AGAAAAATCA	360
AAACTCAAGC	AACGCCAACG	TTGAATGGCA	ATGGGCTCTT	GAGCGGCAAT	CCAAATGGCG	420
GAGGCGGTGA	CTCCTCGCCC	AGCCATGAAG	TGGACCATCC	GGGTGGAGCA	CAAGGAGCTC	480
AAGCAGCAGG	AGGCTTGCCA	TCTTTAAGTG	GCACGCCATT	GAGGCACCAC	AAGCGCGCCA	540
GTATCTCCAC	AGCATCGCCT	CCAATTCGCG	AACGGCGTGG	CACCAACACC	AGCATCGTGG	600
TCGAACTGGA	TGGCAGTGGC	AGCGGGAGTG	GGAGTGGCGG	TGGTGGCGTT	GGCGTTGGTC	660
AGGGTGCGGG	TTGTCTCTCC	TCGGGCAGCT	GCACTGCGTC	CGGAAAAAGT	TCGCGGGAAC	720
TATCGCCGTC	GCCGAAAAAC	CAACAGCAGC	CCAGAAAGAT	GTCACAGGAT	TATCGGTGCG	780
GTGCCGGCAG	CTTTATGCAC	CTGGACGACG	AGGGACGCAG	TCTGCTGATG	CGCAAGCCGA	840

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TGAGACTGAA	GAACATCGAG	GGCAGGCCGG	AGGTCTACGA	CACGCTGCAC	TGCAAGGGTC	900
GCGAGATTCT	TTCCTGCTCG	AAGGCCACCT	GTACGAGCAG	CATTATGAAC	ATTGGCAATG	960
CGGCGGTGGA	GGCCAGGAAA	TCCGATCTGA	TCCTCGAACA	CGCCAAGGAC	TTCCTCGAGC	1020
AGTACTTTAC	ATCGATAAAG	CGTACATCAT	GTACCGCCCA	CGAGACGCGA	TGGAAACAGG	1080
TGCGCCAGAG	CATTGAGACC	ACTGGACACT	ATCAGCTAAC	CGAAACGGAG	CTAATTTATG	1140
GTGCCAAATT	GGCCTGGCGC	AATTCTTCAC	GTTGCATTGG	CCGAATACAA	TGGTCGAAGT	1200
TGCAGGTCTT	TGACTGTCGT	TATGTGACAA	CAACAAGTGG	CATGTTTGAA	GCCATTTGCA	1260
ATCACATTAA	ATATGCAACA	AATAAGGGCA	ACCTGAGATC	GGCCATCACG	ATATTTCCAC	1320
AACGCACAGA	TGCCAAGCAT	GATTATCGCA	TTTGAATAA	CCAATTAATA	TCTTATGCCG	1380
GCTACAAGCA	GGCGGATGGA	AAAATCATTG	GCGATCCCAT	GAATGTGGAG	TTTACAGAGG	1440
TCTGCACCAA	GCTGGGCTGG	AAGAGCAAGG	GCAGCGAGTG	GGACATACTG	CCATTGGTGG	1500
TCTCGGCCAA	TGGTCACGAT	CCGGACTACT	TTGATTACCC	GCCCGAATTG	ATACTGGAAG	1560
TTCCGCTGAC	CCATCCCAA	TTCGAATGGT	TCTCGGATCT	GGGACTGCGA	TGGTACGCCC	1620
TGCCCCCGCT	ATCCAGTATG	CTGTTTCGATG	TGGGCGGCAT	TCAGTTTACG	GCCACCACAT	1680
TCAGTGGTTG	GTACATGTGG	ACAGAGATTG	GCAGCCCGAA	TTTATCGGAC	ACAAATCGCC	1740
GCAATATGCT	GGAGACGGTG	GCGCTGAAGA	TGCAACTGGA	CACCCGTACG	CCCACATCCT	1800
TGTGGAAGGA	CAAGGCTGTG	GTGGAGATGA	ACATTGCCGT	GCTCCACTCC	TACCAGAGTC	1860
GCAACGTGAC	CATTGTGGAT	CACCACACGG	CCAGCGAGAG	CTTTATGAAG	CATTTCGAGA	1920
ACGAGTCCAA	GCTCAGGAAT	GGGTGTCCCG	CTGATTGGAT	TTGGATCGTG	CCGCCGCTGT	1980
CGGGCTCCAT	AACGCCGGTA	TTCCATCAGG	AGATGGCTCT	GTACTACCTG	AAGCCCTCGT	2040
TCGAGTACCA	GGATCCCGCC	TGGCGAACCC	ACGTGTGGAA	AAAGGGGCGT	GGCGAGAGCA	2100
AGGGCAAGAA	GCCAAGACGT	AAATTCAATT	TTAAACAAAT	CGCTAGGGCT	GTGAAATTTA	2160
CATCGAAACT	ATTTGGACGC	GCCTTATCGA	AACGCATAAA	GGCAACAGTT	CTATATGCCA	2220
CCGAAACTGG	CAAATCGGAG	CAGTATGCGA	AGCAACTTTG	TGAACTCCTA	GGGCACGCAT	2280
TCAATGCACA	GATATATTGC	ATGTCCGACT	ACGATATATC	CTCCATTGAG	CACGAGGCAT	2340
TGTTAATTGT	TGTGGCCTCC	ACCTTTGGCA	ACGGTGATCC	CCCCGAAAAC	GGCGAGCTTT	2400
TCTCCCAGGA	ATTGTATGCG	ATGCGTGTCC	AGGAGTCTTC	CGAGCATGGA	TTGCAGGACT	2460
CCAGCATTGG	CTCGTCAAAG	TCCTTCATGA	AGGCCAGCTC	GCGGCAGGAG	TTCATGAAGC	2520
TGCCACTGCA	ACAGGTGAAG	AGAATCGACC	GATGGGACTC	GCTGCGGGGC	TCCACCTCGG	2580
ACACCTTCAC	CGAGGAGACC	TTTGGTCCCC	TCTCCAATGT	CCGGTTTGCC	GTTTTTGCCC	2640
TCGGCTCCTC	GGCCTATCCA	AATTTCTGCG	CCTTCGGTCA	GTATGTGGAC	AACATTCTGG	2700

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GCGAGCTGGG	CGGCGAACGC	CTGCTGAGGG	TGGCCTACGG	CGACGAGATG	TGCGGACAGG	2760
AGCAGTCGTT	CCGGAAGTGG	GCGCCCGAGG	TATTCAAGTT	GGCCTGCGAG	ACCTTCTGCC	2820
TGGATCCAGA	GGAGAGCCTT	TCGGATGCCT	CGCTAGCCCT	GCAGAACGAT	TCGCTGACTG	2880
TGAATACGGT	GCGCCTGGTG	CCGTCCGGCA	ATAAGGGATC	CCTGGACAGC	AGTTTATCCA	2940
AGTACCACAA	CAAGAAGGTG	CACTGCTGCA	AGGCGAAGGC	GAAGCCCCAC	AATTTGACCC	3000
GTTTGAGTGA	GGGAGCCAAG	ACAACGATGC	TGCTGGAGAT	CTGTGCACCT	GGCTTGAGT	3060
ACGAGCCGGG	TGATCATGTG	GGCATCTTTC	CGGCGAATCG	AACGGAACTG	GTCGACGGAC	3120
TGCTAAATCG	ACTGGTGGGT	GTGGATAATC	CCGACGAGGT	GCTGCAGTTG	CAATTGCTAA	3180
AGGAAAAGCA	GACATCGAAT	GGTATATTCA	AGTGCTGGGA	GCCGCACGAC	AAAATACCGC	3240
CGGATACTCT	AAGGAATCTA	CTGGCCCCGAT	TCTTTGATCT	GACCACTCCG	CCATCGCGAC	3300
AGCTACTCAC	CCTGCTGGCT	GGATTCTGTG	AGGACACCGC	GGACAAGGAG	CGGCTGGAGT	3360
TGCTGGTCAA	CGATTCTGCG	GCCTACGAGG	ACTGGCGGCA	CTGGCGGCTG	CCGCACCTGC	3420
TGGACGTCCT	CGAGGAGTTC	CCTTCGTGCC	GACCACCGGC	TCCCCTTCTG	CTTGCCCAAC	3480
TAACGCCGCT	GCAGCCTCGC	TTCTATTCCA	TTTCCTCGTC	GCCGCGCCGC	GTTAGTGACG	3540
AAATCCACCT	GACGGTGGCC	ATCGTGAAGT	ACCGTTGTGA	AGATGGTCAG	GGTGACGAGC	3600
GGTACGGCGT	GTGCTCTAAC	TATCTATCCG	GCTTGCGGGC	AGACGACGAG	CTGTTTATGT	3660
TCGTGAGAAG	CGCCTTGGGC	TTCCATTTCG	CCAGCGATCG	GAGTCGTCCC	ATTATTCTGA	3720
TTGGTCTCTG	CACAGGAATA	GCTCCATTCC	GCTCCTTTTG	GCAGGAGTTC	CAGGTGCTAC	3780
GCGACCTTGA	TCCCACGGCC	AAATTGCCCA	AGATGTGGCT	CTTCTTTGGC	TGCCGGAATC	3840
GGGATGTGGA	CTTGTACGCC	GAGGAGAAGG	CAGAGCTACA	GAAGGATCAA	ATCCTAGACC	3900
GAGTTTTTCT	CGCTCTGTCC	AGGGAGCAGG	CCATTCCGAA	GACATATGTG	CAGGACCTGA	3960
TTGAGCAGGA	ATTCGATTTC	TTGTACCAGT	TGATTGTCCA	GGAGCGGGGC	CACATCTACG	4020
TCTGCGGCGA	TGTCACAATG	GCCGAGCATG	TGTACCAGAC	CATCAGGAAG	TGCATTGCCG	4080
GCAAAGAGCA	GAAAAGCGAG	GCGGAAGTTG	AGACATTTTT	GCTAACACTG	CGGGACGAAA	4140
GTCGCTACCA	CGAGGACATC	TTTGGCATCA	CGCTGCGAAC	GGCTGAGATA	CACACAAAGT	4200
CAAGGGCCAC	GGCCAGGATA	CGAATGGCCT	CCCAGCCCTA	AGGATAGATA	TTCGAAGTAA	4260
TCAAAATAGG	AGGGTGACAT	ATCCAAATTC	GAGAGGAATA	CCAAGCACTT	GCTCTTTTTT	4320
TTCTTCCATA	TTCAAATGCA	ATTAAATATT	GTCGCTTTGT	TCATTACATA	TTCGTATGAA	4380
TAACGTTTAA	ATAAATTACA	TTTTATTATT	GATTCTAATG	TACAAATCAA	TTGTGAAATC	4440
AAAATCTAAA	TGTTAAAATA	TATTTCAAAT	AAACGAATCG	AAAAGGAATT	C	4491

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CLAIMS

What is claimed is:

1. A method of regulating long term memory in an animal comprising inducing of expression of a dCREB2 gene or functional fragment thereof in the animal.
2. The method of Claim 1 wherein the dCREB2 gene encodes a cyclic 3',5'-adenosine monophosphate responsive activator isoform and inducing of said gene results in the potentiation of long term memory.
3. The method of Claim 2 wherein the activator isoform is dCREB2-a or an analogue thereof.
4. The method of Claim 2 wherein induction of the dCREB2 gene encoding a cyclic 3',5'-adenosine monophosphate responsive activator isoform activates the production of a protein which is necessary for the formation of long term memory.
5. The method of Claim 4 wherein the activator isoform is dCREB2-a or an analogue thereof.
6. The method Claim 1 wherein the dCREB2 gene encodes a repressor isoform and inducing of said gene results in the blocking of long term memory.
7. The method of Claim 6 wherein the repressor isoform is dCREB2-b or an analogue thereof.

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8. A method of regulating long term memory in an animal comprising inducing repressor and activator isoforms of dCREB2 wherein long term memory is potentiated in the animal when the net amount of functional activator (ΔC) is greater than zero.
- 5
9. The method of Claim 8 wherein the repressor isoform is dCREB2-b or an analogue thereof and the activator isoform is dCREB2-a or an analogue thereof.
10. A method of identifying a substance capable of affecting long term memory in an animal comprising the determination that said substance alters the induction or activity of repressor and activator isoforms of dCREB2 from normal in the animal.
- 10
11. A method of enhancing long term memory formation in an animal comprising increasing the level of activator homodimer from normal in an animal.
- 15
12. The method of Claim 11 wherein the activator homodimer is a dCREB2a homodimer.
13. A method of enhancing long term memory formation in an animal comprising decreasing the level of activator-repressor heterodimer from normal in an animal.
- 20
14. The method of Claim 13 wherein the activator-repressor heterodimer is a dCREB2a-dCREB2b heterodimer.
15. A method of enhancing long term memory formation in an animal comprising decreasing the level of repressor homodimer from normal in an animal.
- 25

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16. The method of Claim 15 wherein the repressor homodimer is a dCREB2b homodimer.
17. A method of identifying a substance capable of affecting long term memory in an animal comprising the determination that said substance alters from normal, in the animal, the formation of a dimer selected from the group consisting of: activator homodimer, activator-repressor heterodimer and repressor homodimer.
18. Isolated DNA encoding a cyclic 3',5'-adenosine monophosphate responsive transcriptional activator.
19. The isolated DNA of Claim 18 wherein the cyclic 3',5'-adenosine monophosphate responsive transcriptional activator is encoded by a *Drosophila* dCREB2 gene.
20. The isolated DNA of Claim 18 wherein the *Drosophila* dCREB2 gene codes for a dCREB2-a isoform.
21. The isolated DNA of Claim 18 which hybridizes to DNA having the sequence in Figure 1A (SEQ ID NO.: 1).
22. The isolated DNA of Claim 18 which encodes the amino acid sequence in Figure 1A (SEQ ID NO.: 2).
23. Isolated DNA encoding an antagonist of cyclic 3',5'-adenosine monophosphate-inducible transcription.
24. The isolated DNA of Claim 23 wherein the antagonist of cyclic 3',5'-adenosine monophosphate-inducible transcription is encoded by a *Drosophila* dCREB2 gene or a functional fragment thereof.

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25. The isolated DNA of Claim 24 wherein the *Drosophila* dCREB2 gene codes for a dCREB2-b isoform.
26. An isolated DNA which encodes a *Drosophila* dCREB2 gene or a functional fragment thereof.
- 5 27. The isolated DNA of Claim 26 wherein the *Drosophila* dCREB2 gene codes for an isoform selected from the group consisting of:
- a) dCREB2-a;
 - b) dCREB2-b;
 - 10 c) dCREB2-c; and
 - d) dCREB2-d.
28. The isolated DNA of Claim 26 wherein the *Drosophila* dCREB2 gene codes for an isoform selected from the group consisting of:
- 15 a) dCREB2-q;
 - b) dCREB2-r; and
 - c) dCREB2-s.
29. Isolated DNA encoding an enhancer-specific activator.
- 20 30. The isolated DNA of Claim 29 wherein the enhancer specific activator is encoded by a *Drosophila* dCREB1 gene or a functional fragment thereof.
31. The isolated DNA of Claim 30 which hybridizes to DNA having the sequence in Figure 5 (SEQ ID NO.: 7).
- 25 32. The isolated DNA of Claim 30 which encodes the amino acid sequence in Figure 5 (SEQ ID NO.: 8).
33. Isolated DNA encoding a nitric oxide synthase of *Drosophila* (DNOS).

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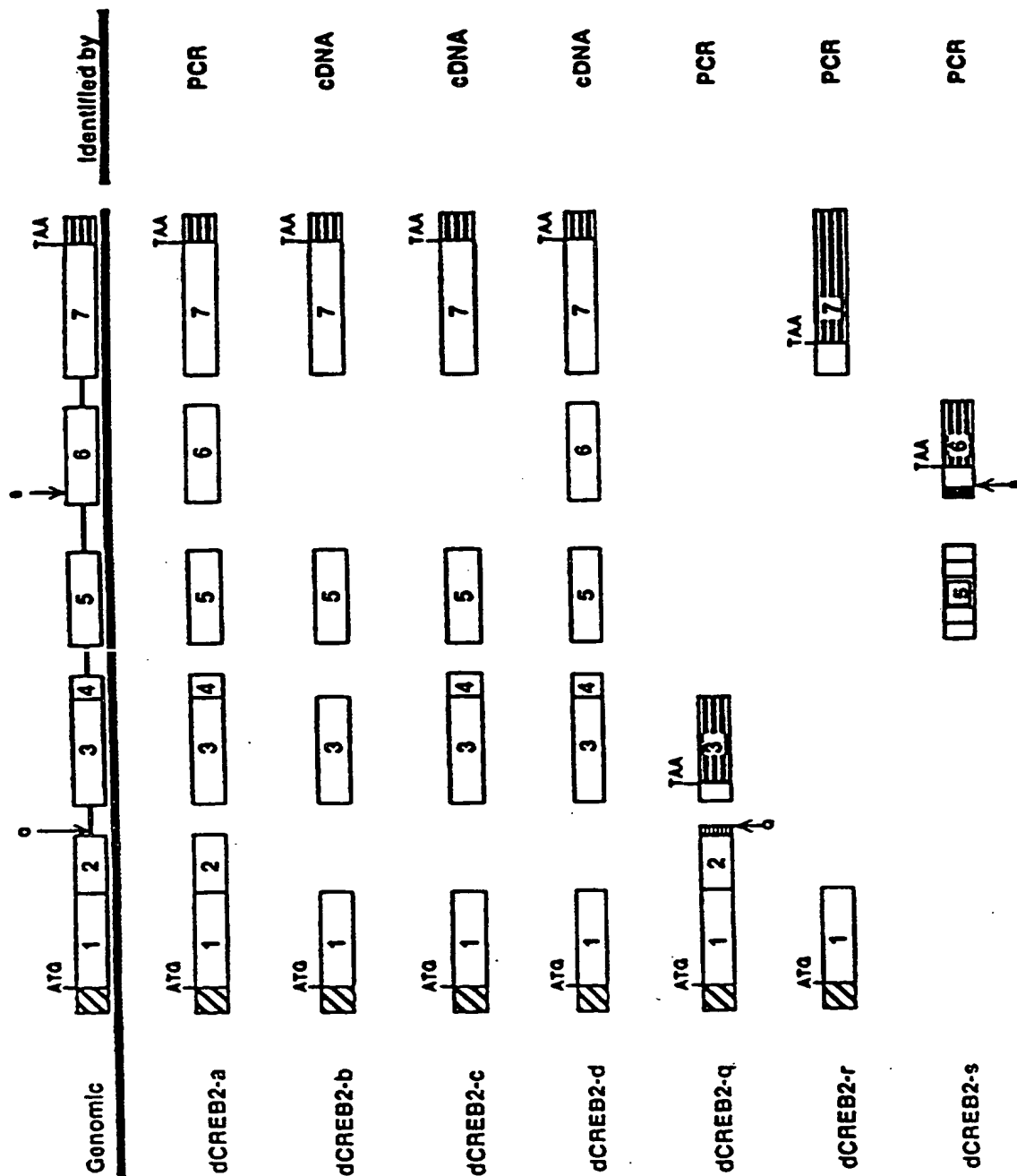
34. The DNA of Claim 33 encoding a DNOS of neuronal locus.
35. The DNA of Claim 33 encoding a DNOS which contains putative heme, calmodulin, FMN, FAD and NADPH binding site domains.
- 5 36. A method for assessing the effect of a drug on long term memory formation comprising:
- a) administering said drug to *Drosophila*;
 - b) subjecting the *Drosophila* to classical conditioning and to at least one odorant and electrical shock; and
 - 10 c) assessing the performance index of said classical conditioning,
- wherein the effect of said drug occurs when said drug alters said performance index from normal.
- 15 37. A method of Claim 36 wherein said drug affects long term memory formation by altering the induction or activity of repressor and activator isoforms of dCREB2.

dCREB2
 CREB
 CREM 1
 ATF-1

AKREALNKHREAREACRAKKKKYKCLEHRAVAULEHQNKHLEELKKEIYC
 AKREVALNKHREAREACRAKKKKYKCLEHRAVAULEHQNKTLEELKALKDLYC
 AKRELRLNKHREAREACRAKKKKYKCLEHRAVAULEHQNKTLEELKALKDLYC
 LKREIRLNKHREAREACRAKKKKYKCLEHRAVAULEHQNKTLEELKALKDLYS

FIGURE 1B

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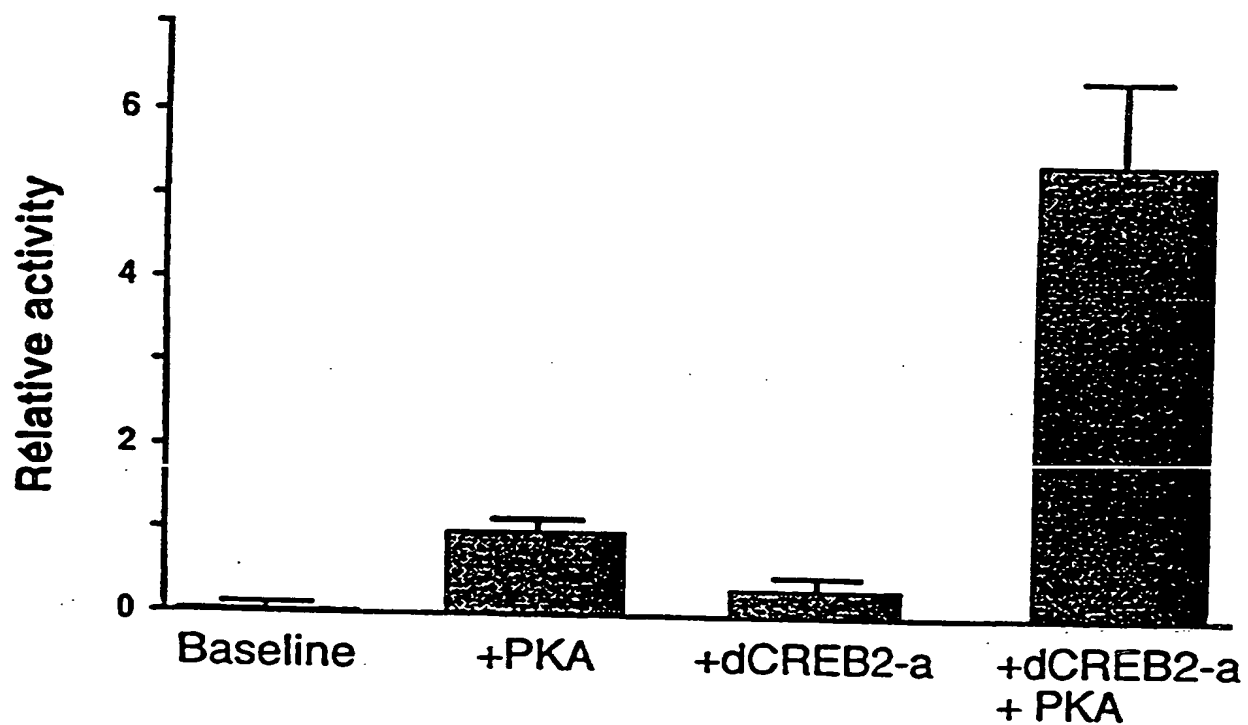


Key: = coding sequences. = 5' untranslated sequences. = 3' untranslated sequences. = coding sequence excluded by alternative splicing. = portion of exon included in spliced transcript is unknown.

Figure 2

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Figure 3



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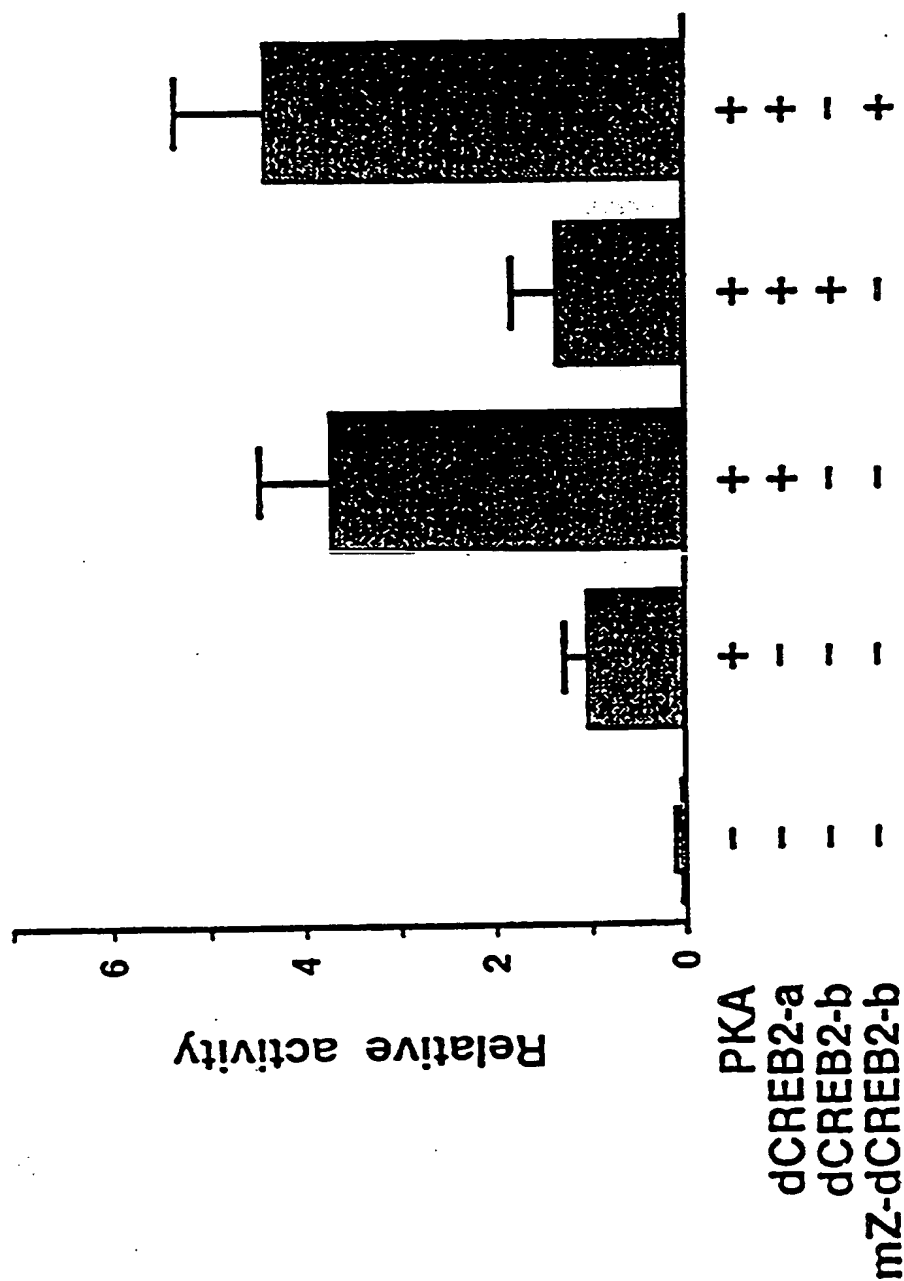


Figure 4

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1 ATGTTACTCGGAGAAATATGTTTTCTACTTTACATCGTTAGATGCTGCTACCGCTACA
 1 N L L G E H N F S T F T S L D A A T A T
 61 ACCAACACCGGTGAATTCTTAATGAATGAATCTCCAGGCCAGAGCCCGGTGACTTAATG
 21 T H T G E F L N H E S P A Q E A G D L N
 121 TTGGATAGTCTGGATTTCACATTATGGGCGAAACCTGGCAGATGATTTCCAGACCTCG
 41 L D S L D F N I N G E H L A D D F Q T S
 181 GCTTCACAGCTTCGGAGGACAGATGACTCCTTTCGTTGTTGATACCAATGTTTTGAA
 61 A S P A S E D K N T P F U U D T H U F E
 241 TCCGTCTTCAGAACACCGAAGATACCTTCTAGGAGATATCGACAAATGTTGGTATTGTT
 81 S U F K N T E D T L L G D I D H U G I U
 301 GACACGGAGTTGAAGGAGATGTTGATTTGCTTGACTCGGAATCAATAACGGCACTCCT
 101 D T E L K E N F D L U D S E I N H G T P
 361 ATCAGCAGGAGAGAAAGGATGATTTGGAATTTACTTCAAGATCCCACTCCACCTCAGCT
 121 I K Q E E K D D L E F T S R S Q S T S A
 421 CTCTTGTCGTCGAATCGACTTCTGCTTCTCCAGCTGATGCTGCCGCTGCATGTGCAAGT
 141 L L S S K S T S A S P A D A A A A C A S
 481 CCTTCGTCATCGTCTTGTAAGATCCTATTCTTCTGCTCAGCTAGAACTACGGGTTCC
 161 P S S S S C K A S Y S S A Q L E T T G S
 541 GATGCTCCAAGAAAGATAAGCTGGGCTGCACCCCTTACCTAGAAACAGAGAAACAA
 181 D A P K K D K L G C T P Y T A K Q R N H
 601 CCATTACCTCCGGTCATTCCAAAGGTCAGGATGTTGCTTCTATGAAAGGGCAGAAAC
 201 P L P P U I P K G Q D U A S N K R A R N
 661 ACTGAGGCCGCAAGAGATCAGAGCCAGAAAAATGGAAGAAATGTCCCACTTGAGAA
 221 T E A A R R S R A R K N E R M S Q L E E
 Basic region →
 721 AAGTGTCAAAGCTTGTGAGGAAACGACGACTTGAAAGCTCAGTTCAAGCTTTGAAG
 241 K C Q S L L K E N D D L K A Q U Q A L K
 zipper →
 781 AATTACTTGGACACAA
 261 K L L G Q Q

FIGURE 5

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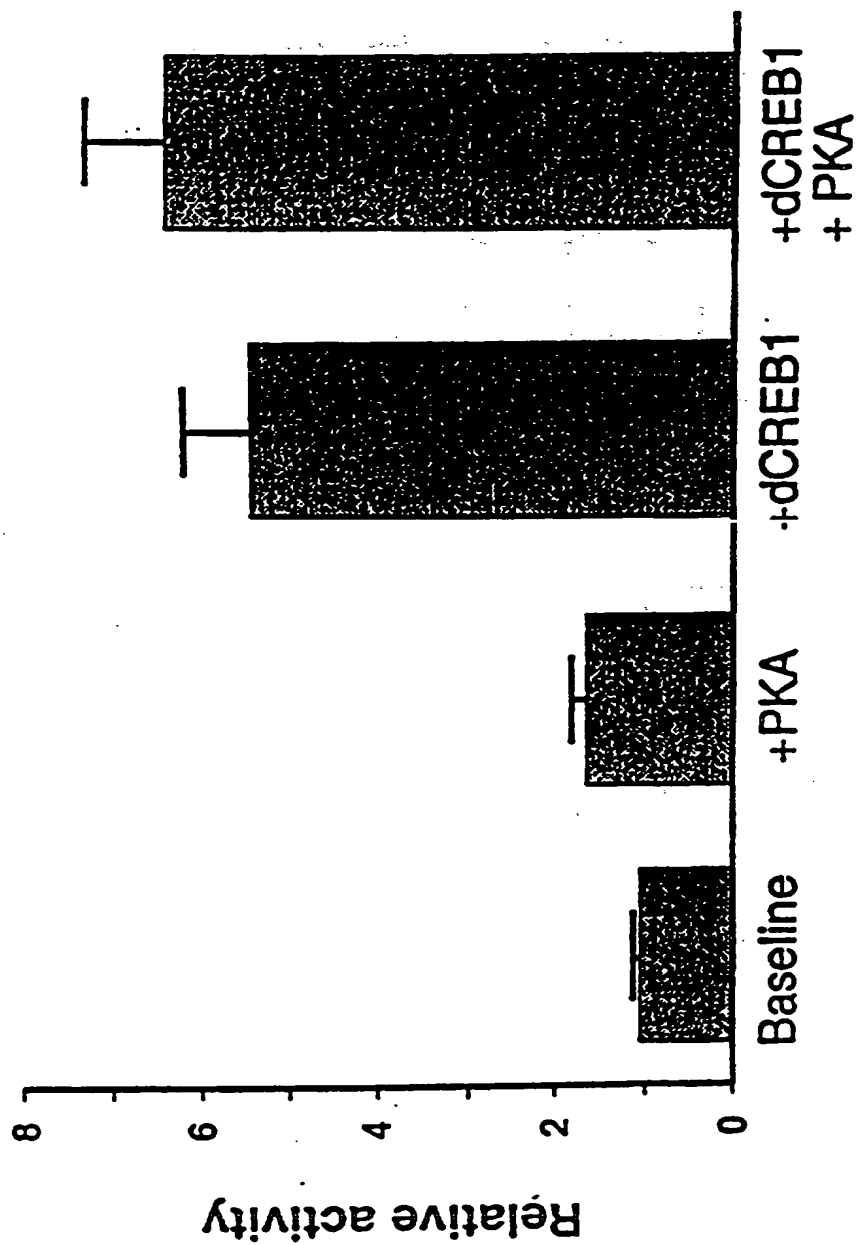


Figure 6

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LANE #	1	2	3	4	5	6
HEAT SHOCK	-	-	+	+	+3	+3
FLIES	wt	CREB	wt	CREB	wt	CREB

FIG. 7A



— CREB TRANSGENE
RNA

LANE #	1	2	3	4	5	6	7	8	9	10	11	12
HEAT SHOCK	-	-	+	+	+1	+1	+3	+3	+9	+9	+24	+24
FLIES	wt	CREB	wt	CREB	wt	CREB	wt	CREB	wt	CREB	wt	CREB

FIG. 7B



— dCREB 28
PROTEIN

lane	1	2	3	4	5	6	7	8
blocker	wt	m	wt	m	wt	m	wt	m
hs	-	-	+	+	+3	+3	+6	+6

FIG. 7C



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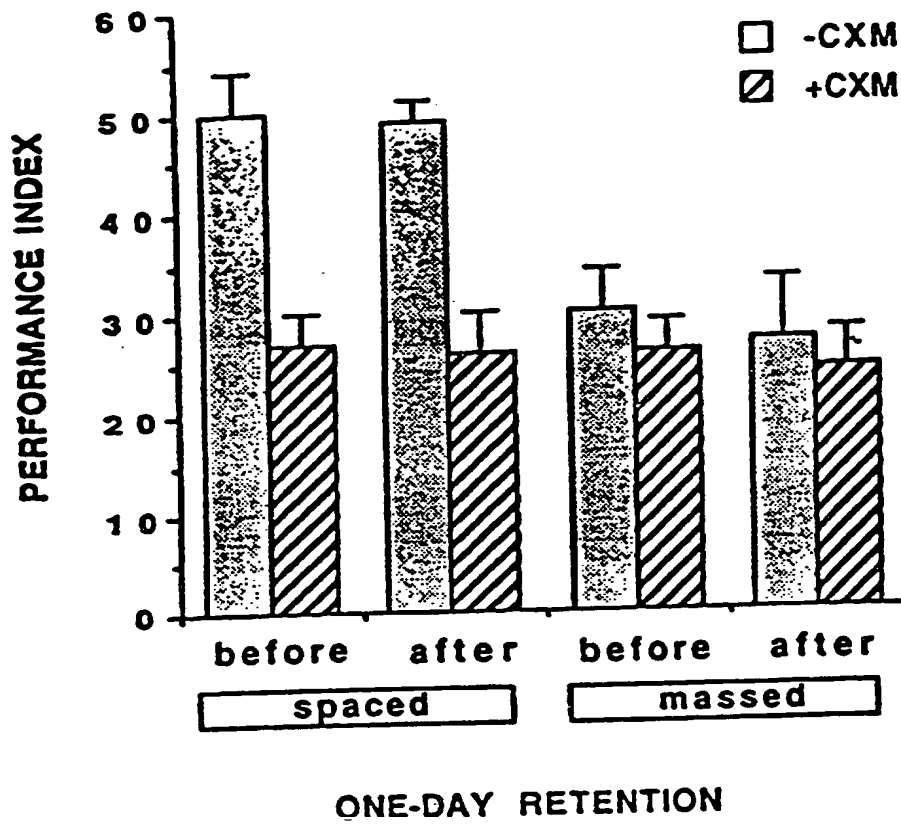


Figure 8

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Figure 9A

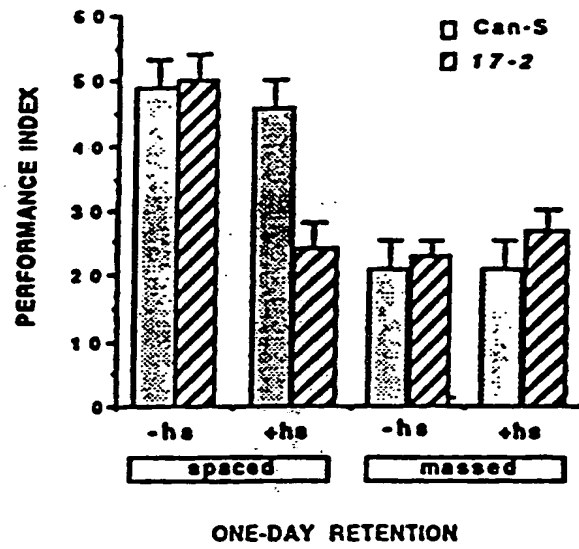


Figure 9B

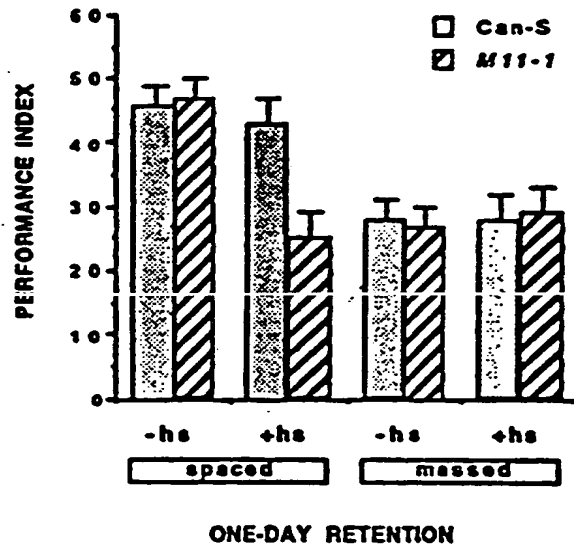
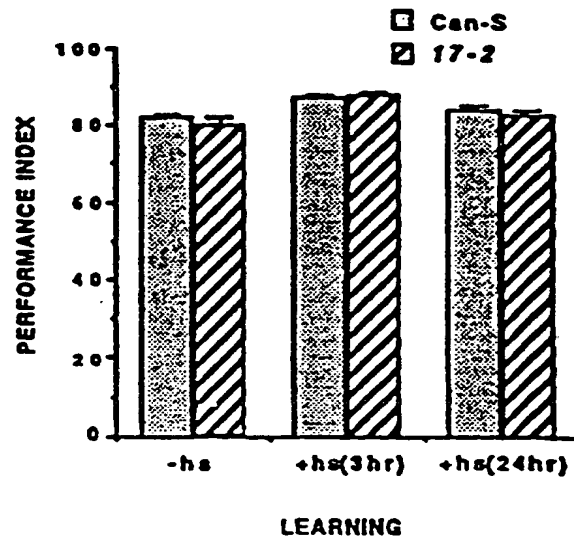


Figure 9C



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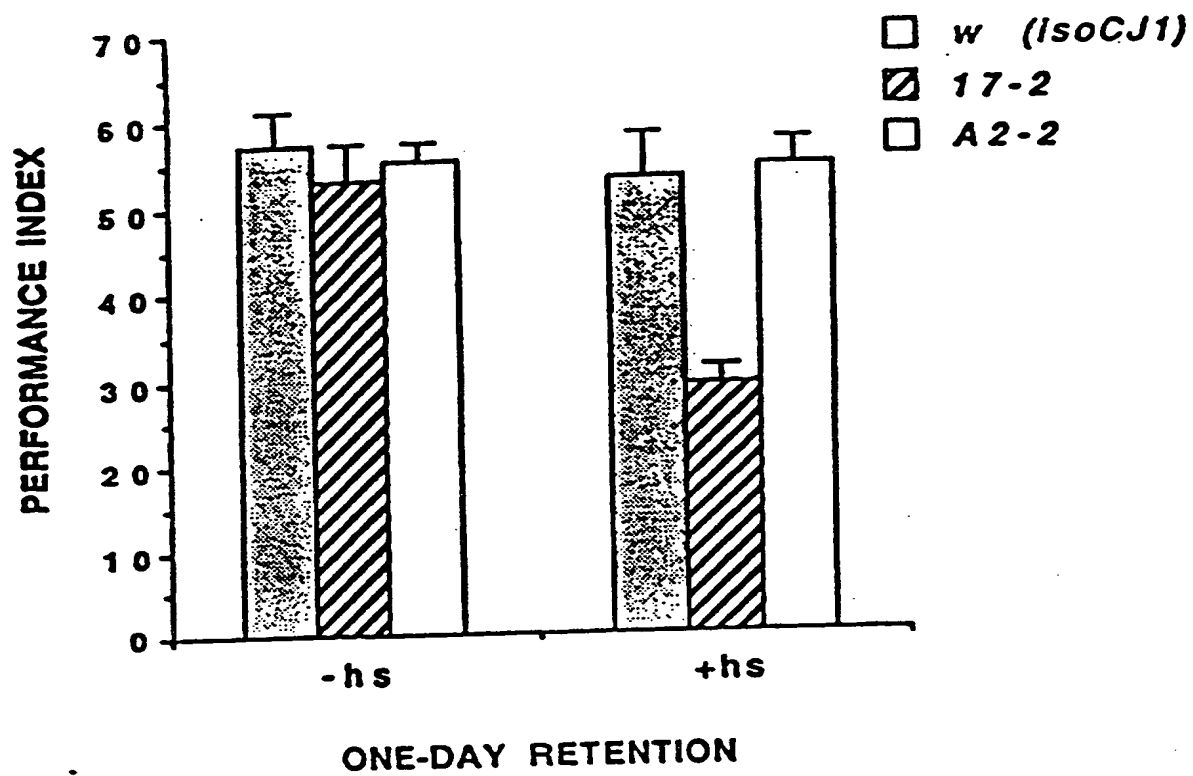


Figure 10

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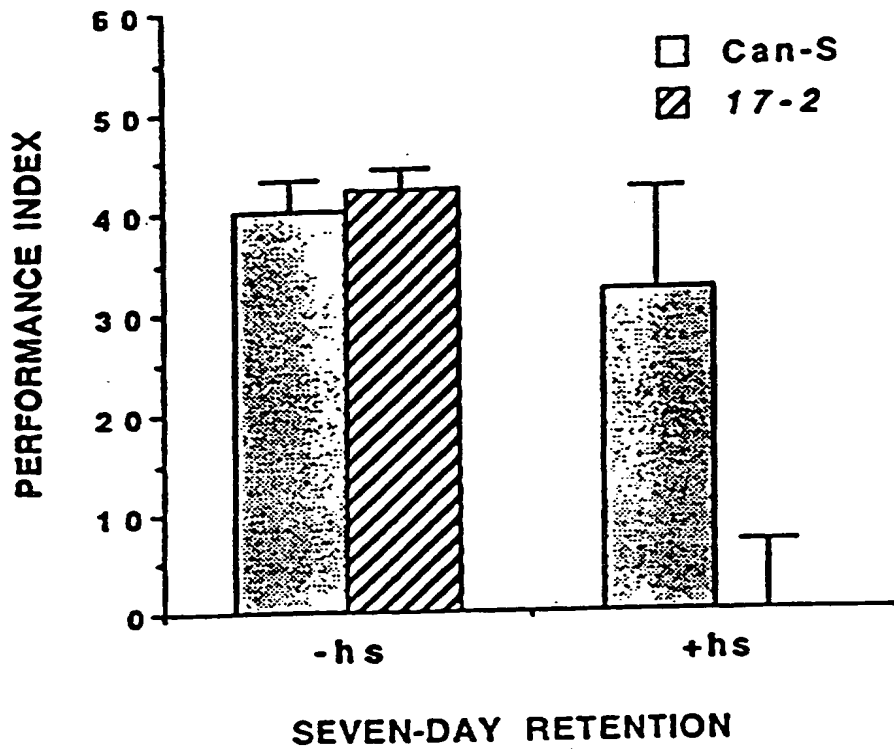


Figure 11

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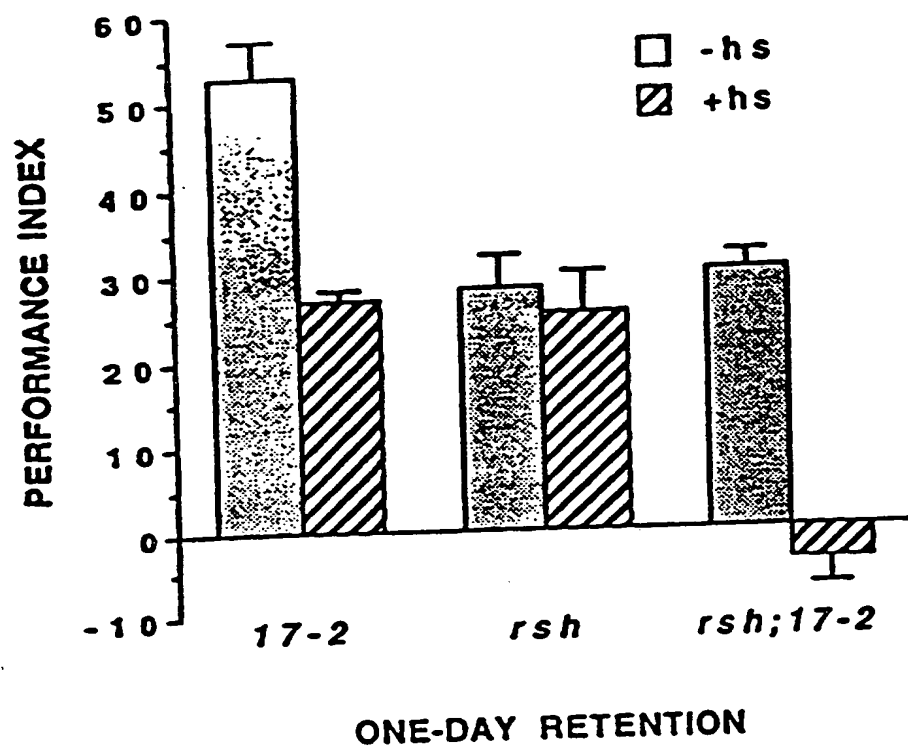


Figure 12

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Figure 13A

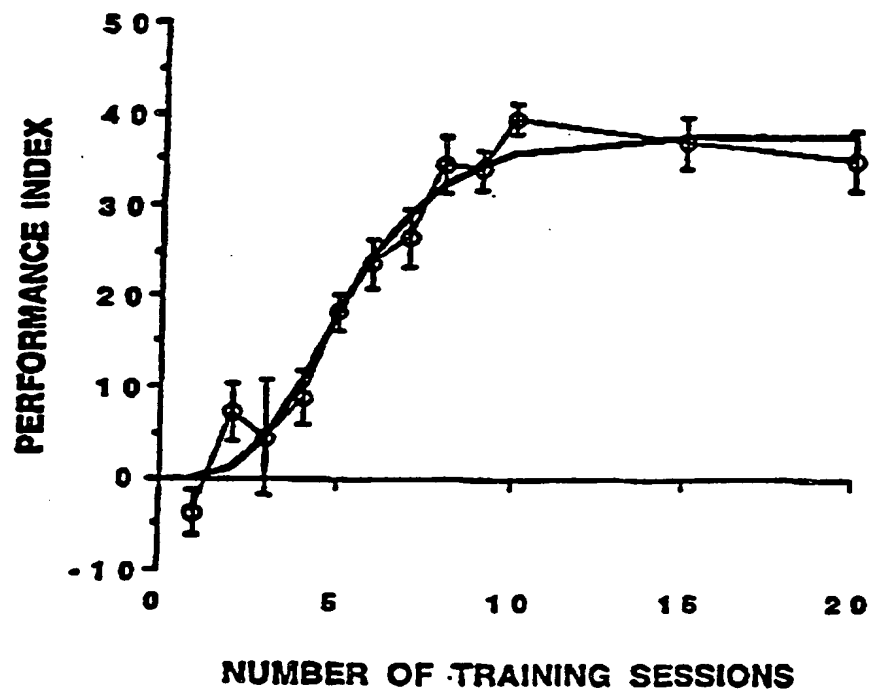
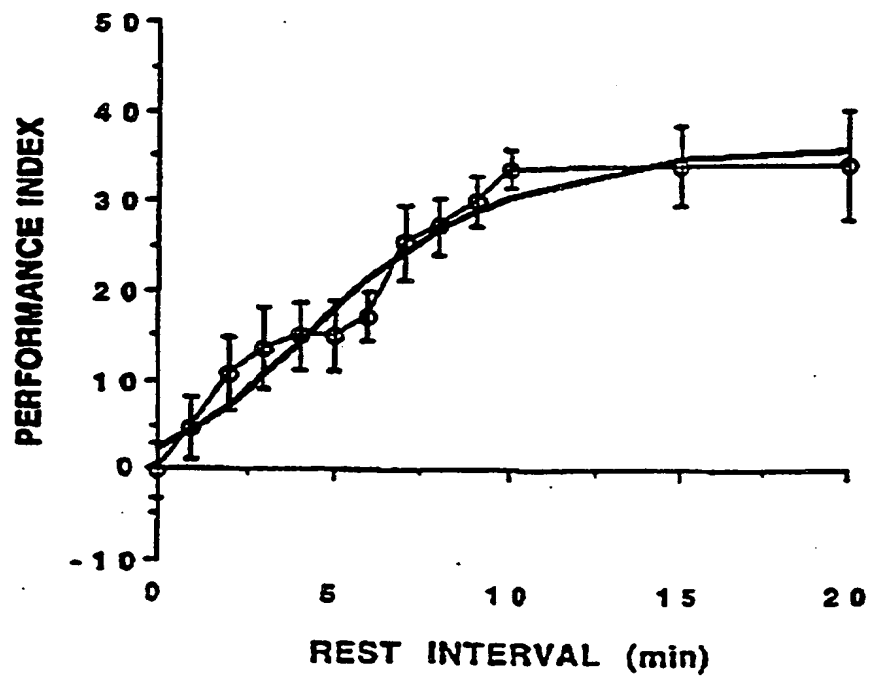


Figure 13B



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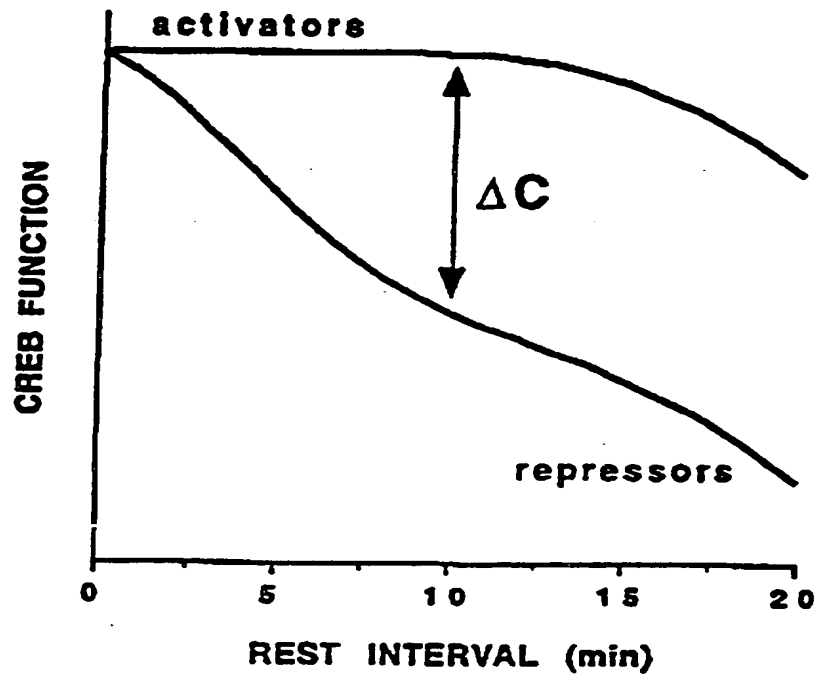


Figure 14

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Figure 15A

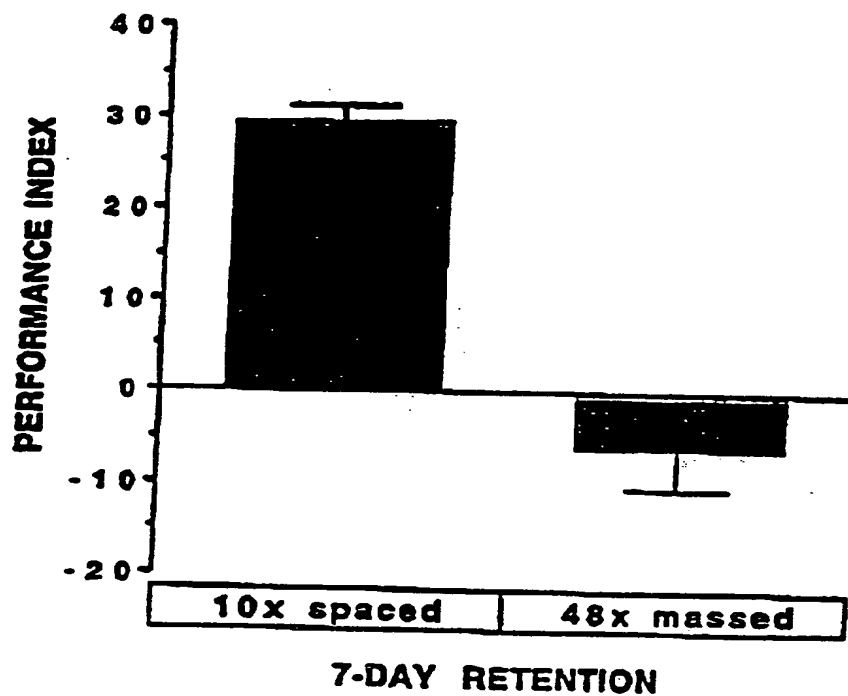
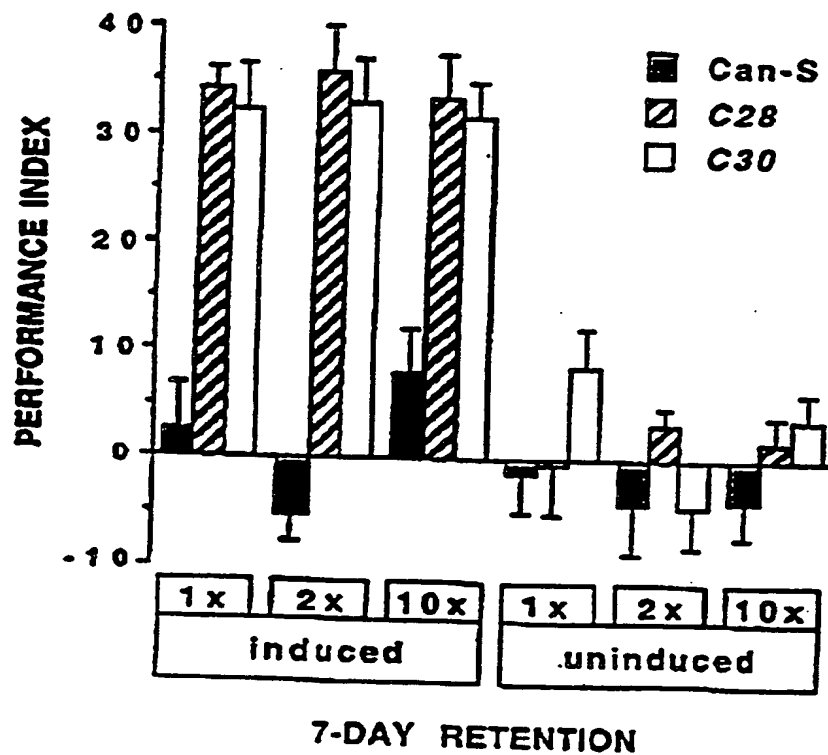


Figure 15B



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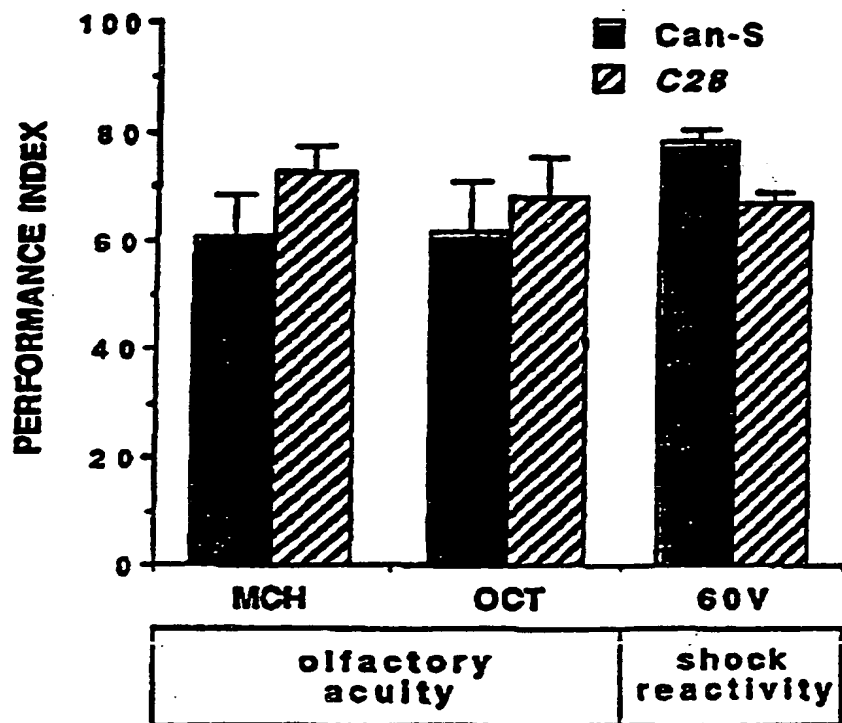


Figure 15C

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Figure 16A

DNOS	MSQ-----H	PTSIFENLRF	VTIKRATRAQ	QQQQQQQQQQ	L-----	35
BENOS	MGN-----	-----L	--KSVC--	--QE--PGPP	-----	14
RNNOS	MEENTFGVQQ	IQPNVISVRL	FKRVGGLGF	LVKERVSKPP	VTISDLIRGG	50
MMNOS	MAC-----	-----PWKFL	FKVKSJ----	--QSDLKEEK	-----	22
DNOS	QQQQQQLOQQ	-----	-----KAQTQ	QQNSRKIKTQ	ATPTLNGNGL	70
BENOS	-----CGL--	-----	-----G	L----GLG--	-----LGLOGK	28
RNNOS	AAEQSGLIQA	GDIILAVNDR	PLVDLSYDSA	LEVLRGIASE	THWVLIIRGP	100
MMNOS	-----DI---	-----	-----N	N----NVK--	-----KTPCAV	35
DNOS	LS-GNPNGCG	GDSSPSHEVD	HPGGAQGAQ-	-----	-----AAG	101
BENOS	QG-----	-PASPAPEPS	RAPAPATP--	-----	-----	47
RNNOS	EGFTTHLETT	FTGDGTPKTI	RVTQPLGPPT	KAVDLSHQPS	ASKDQSLAVD	150
MMNOS	LS-----	PTIQDDPKSH	QNGSPQLL--	-----	-----	55
DNOS	GLPSLSGTPL	RHH-----	---KRASIST	ASPPIRERRG	-----	131
BENOS	-----HAPD	HS-----	-----	-PAPNS----	-----	58
RNNOS	RVTGLGNGPQ	HAQGHGQGAG	SVSQANGVAI	DPTMKSTKAN	LQDIGEHDEL	200
MMNOS	-----TGTA	QN-----	-----	--VPESL--	-----	66
DNOS	--TNTSIVVE	LDGSGSGSGS	GG-----	GGVGVGGQAG	CPPSGSCTAS	171
BENOS	-----PTLT-	-----	-----	-----R---	-----PPEG	67
RNNOS	LKETEPVLSI	LNSGSKATNR	GCPAKAEMKD	TGIQVDRDLQ	GKSHKAPPLG	250
MMNOS	-----DKLHV	-----	-----	-----	-----TSTR	75
DNOS	GKSSRELSPS	PKNQQQPRUM	SQDYRSR---	-AGSFMHLD	EGRSLLMRKP	217
BENOS	-----	-----	-----	-----	-----PKF	70
RNNOS	GDNDRVFNDL	WGKDNVPVIL	NNPYSEKEQS	PTSGKQSPTK	NGSPSRCPRF	300
MMNOS	-----	-----	-----	-----	-----POY	78
DNOS	MRLKNIEGRP	EVYDTLHCKG	REILSCSKAT	CTSSIMN---	-IGNAAVEAR	263
BENOS	PRVKNWELGS	ITYDTLCAQS	QQDGPCTPRR	CLGSLVLPRK	LQTRPSGPP	120
RNNOS	LKVKNWETDV	VLTDTLHLKS	TLETGCTEHI	CMGSIMLPSQ	-HTRKPEDVR	349
MMNOS	VRIKNWGSGE	ILHDTLHKA	TSDFTCKSKS	CLGSIMNPKS	LTRGPRDKPT	128
DNOS	KSDLILEHAK	DFLEQYFTSI	KRTSCTAHET	RWKQVRQSIE	TTGHIYQLTET	313
BENOS	PAEQLLSQAR	DFINQYYSSI	KRSGSQAHEE	RLQEVAAEVA	STGTIHLRES	170
RNNOS	TKDQLFPLAK	EFLDQYYSSI	KRFGSKAHMD	RLEEVNKEIE	STSTYQLKDT	399
MMNOS	PLEELLPHAI	EFINQYYGSF	KEAKIEEHLA	RLEAVTKEIE	TTGTYQLTLD	178
-----Heme-----						
DNOS	ELIYGAKLAW	RNSSRCIGRI	QWSKLQVFDC	RYVTTTSGMF	EAICNHIKYA	363
BENOS	ELVFGAKQAW	RNAPRCVGRI	QWGKLQVFDA	RDCSSAQEMF	TYICNHIKYA	220
RNNOS	ELIYGAKHAW	RNASRCVGRI	QWSKLQVFDA	RDCTTAHGMF	NYICNHVKYA	449
MMNOS	ELIFATKMAW	RNAPRCIGRI	QWSNLQVFDA	RNCSTAQEMF	QHICRHILYA	228
DNOS	TNKGNLRSAL	TIFFPORTDAK	HDYRIWNNQL	ISYAGYKQAD	GKIIGDPMNV	413
BENOS	TNRGNLRSAL	TVFPQAPAGR	GDFRIWNSQL	VRYAGYRQOD	GSVRGDPANV	270
RNNOS	TNKGNLRSAL	TIFFPORTDGK	HDFRVWNSQL	IRYAGYKQPD	GSTLGDPANV	499
MMNOS	TNNGNIRSAI	TVFPQRSQDGK	HDFRLWNSQL	IRYAGYQMPD	GTRGDAATL	278

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DNOS	EFTEVCTKLG	WKSXGSEWDI	LPLVVSANGH	DPDYFDYPPE	LILEVPLTHP	463
BENOS	EITELCIQHG	WTPGNGRFDV	LPLLLQAPDE	APELFVLPPPE	LVLEVPLGAP	320
RNNOS	QFTEICIQQG	WKAPRGRFDV	LPLLLQANGN	DPQLFQIPPE	LVLEVPIRHP	549
MMNOS	EFTQLCIDLG	WKPRYGRFDV	LPLVLQADGQ	DPEVFEIPPD	LVLEVIMEHP	328
DNOS	KFEWFSDLGL	RWYALPAVSS	MLFDVGGIQF	TATTFSGWYM	STEIGSRNLC	513
BENOS	HTGVVRGPGL	RWYALPAVSN	MLLEIGGLEF	SAAPFSGWYM	STEIGTRNLC	370
RNNOS	KFDWFKDLGL	KWYGLPAVSN	MLLEIGGLEF	SACPFSGWYM	GTEIGVRDYC	599
MMNOS	KYEWFQELGL	KWYALPAVAN	MLLEVGGLEF	PACPFNGWYM	GTEIGVRDFC	378
DNOS	DTNRRNMLET	VALKMOLDTR	TPTSLWKDKA	VVENNIAVLH	SYOSRNVTTV	563
BENOS	DPHRYNILED	VAVCMOLDTR	TTSSLWKDKA	AVEINLAVLH	SFQLAKVTTV	420
RNNOS	DNSRYNILEE	VAKKMDLDMR	KTSSLWKDQA	LVEINIAVLY	SFQSDKVTTV	649
MMNOS	DTQRYNILEE	VGRRMGLETH	TLASLWKDRA	VTEINAVLH	SFQKQNVTTM	428
DNOS	DHHTASESFM	KHFENESKLR	NGCPADWIWI	VPPLSGSITP	VFHQEMALYY	613
BENOS	DHHAATVSFM	KHLDNEQKAR	GGCPADWAWI	VPPIYGSLLP	VFHQEMVNYI	470
RNNOS	DHHSATESFI	KHMENEYRCR	GGCPADWVWI	VPPMSGSITP	VFHQEMLNRY	699
MMNOS	DHHTASESFM	KHMONEYRAR	GGCPADWIWL	VPPVSGSITP	VFHQEMLNRY	478
CaM						
DNOS	LKPSFEYQDP	AWRTHVWKKG	RGESKGGKPR	RKFNFKQIAR	AVKFTSKLFG	663
BENOS	LSPAFRYQPD	PWKG---SAT	KGAG---ITR	KK-TFKEVAN	AVKISASLMG	513
RNNOS	LTPSFEYQPD	PWNTHVWKGT	NGTP---TKR	RAIGFKKLA	AVKFSAKLMG	746
MMNOS	LSPFYFYQIE	PWKTHIWQNE	KLRP----RR	REIRFRVLVK	VVFFASMLMR	524
DNOS	RALSKRIKAT	VLYATETGKS	EQYAKQLCEL	LGHAFNAQIY	CMSDYDISSI	713
BENOS	TLMAKRVKAT	ILYASETGRA	QSYAQQLGRL	FRKAFDPRVL	CMDEYDVVSL	563
RNNOS	QAMAKRVKAT	ILYATETGKS	QAYAKTLCEI	FKHAFDAKAM	SMEEYDIVHL	796
MMNOS	KUMASKVRAT	VLFATETGKS	EALARDLATL	FSYAFNTRVV	CHDQYKASTL	574
DNOS	EHEALLIVVA	STFGNGDPPE	NGELFSQELY	AMRVQESSEH	GLQDSSIGSS	763
BENOS	EHEALVLVVT	STFGNGDPPE	NGESFAAALM	EMSGPYNS--	---SPRPEQH	608
RNNOS	EHEALVLVVT	STFGNGDPPE	NGEKFGCALM	EMRHP-----	---NSVQEER	838
MMNOS	EEEQLLLVVT	STFGNGDCPS	NGQTLKKSL-	-----	-----	603
DNOS	KSFMKASSRQ	EFMKLPLQQV	KRIDRWDSL	GSTSDTFTEE	TFGPLSNVRF	813
BENOS	KSYK---IR-	-FNSVS-CSD	PLVSSWRRKR	KESSNT---D	SAGALGTLRF	649
RNNOS	KSYK---VR-	-FNSVS-SYS	DSRKSSGDGP	DLRDNF---E	STGPLANVRF	879
MMNOS	--FM---LR-	-----	ELNH-----	-----	-----TFRY	615
FMN						
DNOS	AVFALGSSAY	PNFCAFGQYV	DNILGELGGE	RLLRVAYGDE	MCGQEQSFRK	863
BENOS	CVFGLGSRAY	PHFCAFARAV	DTRLEELGGE	RLQLQGQDE	LCGQEEAFRG	699
RNNOS	SVFGLGSRAY	PHFCAFAGHAV	DTLLEELGGE	RILKMREGDE	LCGQEEAFRT	929
MMNOS	AVFGLGSSMY	PQFCAFAHDI	DQKLSHLGAS	QLAPTGEDE	LSGQEDAFRS	665
DNOS	WAPEVFKLAC	ETFCLDPEES	--LSDASLAL	QNDSLTVNTV	RLVPSANKGS	911
BENOS	WAKAAFQASC	ETFCVGEEAK	--AAQDIFS	PKRSWKRRQY	RLSAQAEGLQ	747
RNNOS	WAKKVFKAAC	DVFCVGDDVN	IEKPNNLSIS	NDRSWKRNKF	RLTYVAEAPD	979
MMNOS	WAVQTFRAAC	ETFDVRSKHH	--IQIPKRFT	SNATWEPQOY	RLIQSPEPLD	713

Figure 16B

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DNOS	LDSSLKYYHN	KKVHCKAKA	KPH-NLTRL	EGAKTTHLLE	ICAPGLEYEP	960
BENOS	LLPGLIHVHR	RQMFQATVLS	VENLQSSKST	RATILVRLDT	AGQEGLOQYP	797
RNNOS	LTQGLSNVHK	KRVSAARLLS	RQNLQSPKFS	RSTIFVRLHT	NGNQELQYQP	1029
MMNOS	LNRALSSIHA	KNVFTMLRKS	QONLQSEKSS	RTLLLVQLTF	EGSRGPPSYLP	763
-FAD-PPI-						
DNOS	GDHVGIFPAN	RTELVDGLLN	RLVGVDNPDE	VLQLQLLKEK	QTSNGIFKCN	1010
BENOS	GDHIGISAPN	RPGLVEALLS	RVEDPPPPTE	SVAVEQL-EK	GSPGGPPPSW	846
RNNOS	GDHLGVFPGN	HEDLVNALIE	RLEDAPPANH	VVKVEMLEER	NTALGVISNW	1079
MMNOS	GEHLGIFPGN	QTALVQGILE	RVVDCPTPHQ	TVCLEVLDSE	G-----SYW	807
-FAD-ISO-						
DNOS	EPHDKIPPD	LRNLLARFFD	LTTTPSRQLL	TLLAGFCEDT	ADKERLELLV	1060
BENOS	VRDPRLPPCT	VRQALTFFLD	ITSPPSPRL	RLSTLAEAP	SEQQELETLS	896
RNNOS	KDESRLPPCT	IFQAFKYLD	ITTPPTPLQL	QQFASLATNE	KEKQRLVLS	1129
MMNOS	VKDKRLPPCS	LSQALTYFLD	ITTPPTQLQL	HKLARFATDE	TDRQREALG	857
-FAD-ISO-						
DNOS	NDSSAYEDWR	HWRLPHLLDV	LEEFPSCRPP	APLLLAQLTP	LQPRFYSISS	1110
BENOS	QDPRRYEWW	LVRCTPLLEV	LEQFPSPVALP	APLLLTQLPL	LQPRYYSVSS	946
RNNOS	KGLQEYEEWK	WGNPTMVEV	LEEFPSIQMP	ATLLLTQLSL	LQPRYYSISS	1179
MMNOS	Q-PSEYNDWK	FSNNPTFLEV	LEEFPSLHVP	AAFLLSQLPI	LKPRYYSISS	906
-NADPH-Ribose-						
DNOS	SPRRVSDETH	LTVAIVKYRC	EDQGQDERYG	VCSNYLSGLR	ADDELHMFVR	1160
BENOS	APNAHPGEVH	LTVAVLAYRT	QDGLGPLHYG	VCSTWLSQLK	TGDPVPCFIR	996
RNNOS	SPDMYPDEVH	LTVAIVSYHT	RDGEGPVHNG	VCSSWLNRIQ	ADDVVPCFVR	1229
MMNOS	SQDHTPSEVH	LTVAVVTYRT	RDGQGPLHNG	VCSTWIRNLK	PQDPVPCFVR	956
-NADPH-Ribose-						
DNOS	SALGFHLPSD	RSRPILIGP	GTGIAPFRSF	WQEFQVLRDL	DPTAKLPQMW	1210
BENOS	GAPSFRLPPD	PVPCILVGP	GTGIAPFRSF	WQF-RLHDSQ	SKGLAPPHMT	1045
RNNOS	GAPSFHLPRN	PQVPCILVGP	GTGIAPFRSF	WQQ-RQFDIQ	HKGMNCPMV	1278
MMNOS	SVSGFQLPED	PSQPCILIGP	GTGIAPFRSF	WQQ-RLHDSQ	HKGLKGRMS	1005
-NADPH-Ade-						
DNOS	QEF-DSLYQL	IVQERGHYV	CGDVTHAEHV	YQTIKCIAG	KEQKSEAEVE	1308
BENOS	TELAAEVHRV	LCLERGHMFV	CGDVTHATSV	LQTVQRILAT	EGDMELDEAG	1145
RNNOS	EQLAESVYRA	LKEQGHHYV	CGDVTHAADV	LKAIQRIMTQ	OQKLSEEDAG	1378
MMNOS	KQLANEVLSV	LHGEQGHLYI	CGDVTHAADV	ATTLLKKLVAT	KLNLSEEDQVE	1105
-NADPH-Ade-						
DNOS	TFLTLRDES	RYHEDIFGIT	LRTAEI----	--HTKSRTA	RIRMAS----	1348
BENOS	DVIGVLRDQO	RYHEDIFGLT	LRTQEVTSRI	RTQSFSLQER	HLRGAVPWF	1195
RNNOS	VFISRLRDDN	RYHEDIFGVT	LRTYEVNRL	RSESI AFIEE	SKRDADE-VF	1427
MMNOS	DYFFQLKSQK	RYHEDIFGAV	F-SYGA----	-KKGSALEP	--KAT----	1142
-NADPH-Ade-						
DNOS	-----QP					1350
BENOS	DPPGPDTPGP					1205
RNNOS	-----SS					1429
MMNOS	-----RL					1144

FIGURE 16C

SUBSTITUTE SHEET (RULE 26)

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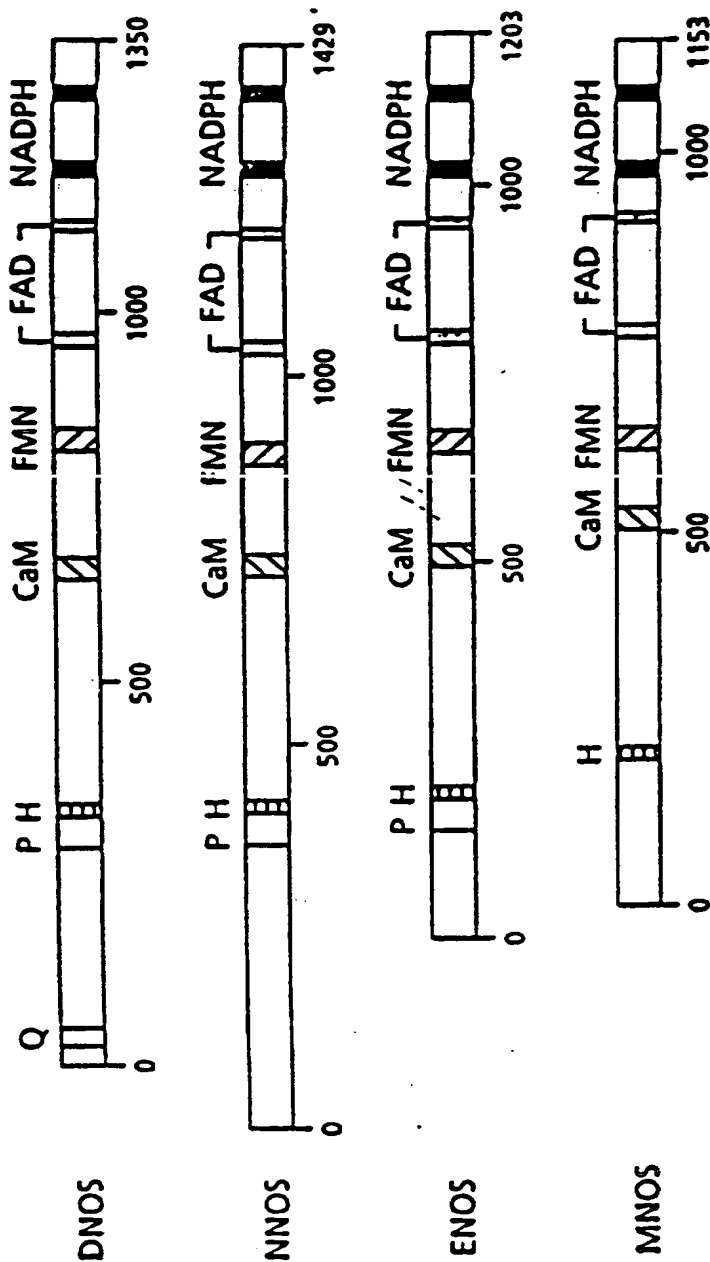


Figure 16D

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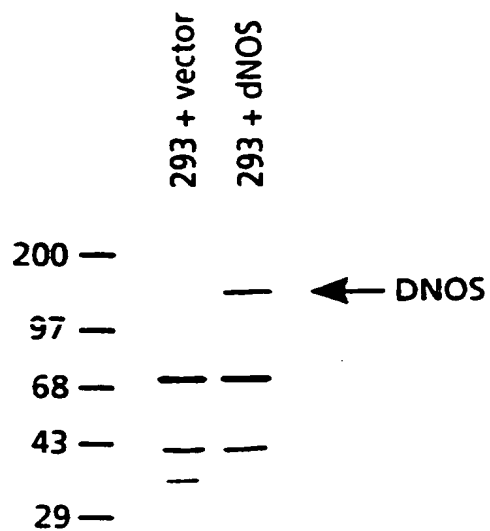


FIG. 17A

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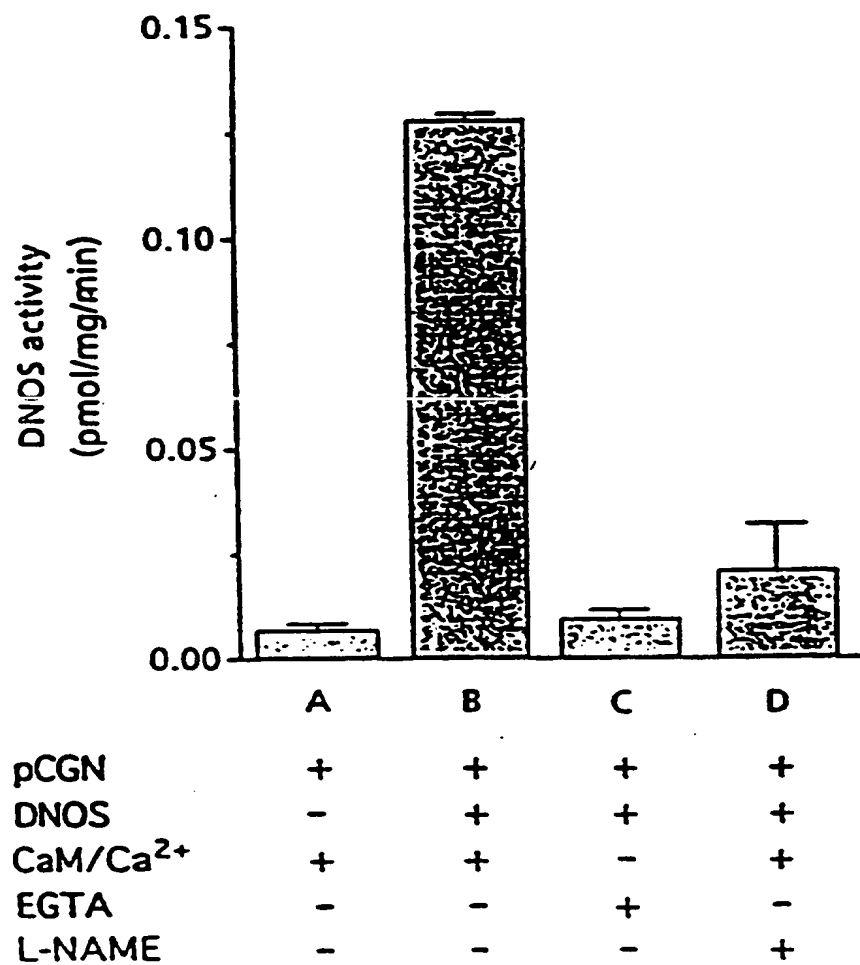


Figure 17B

SUBSTITUTE SHEET (RULE 26)

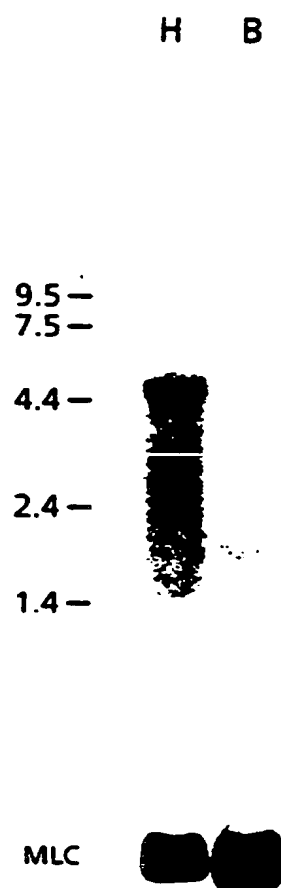


FIG. 18A

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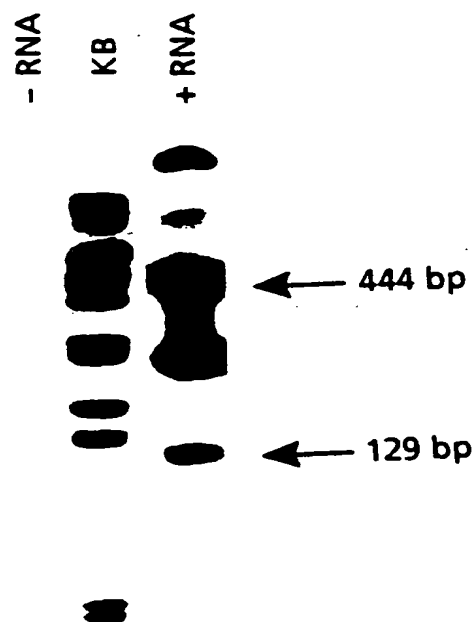


FIG. 18B

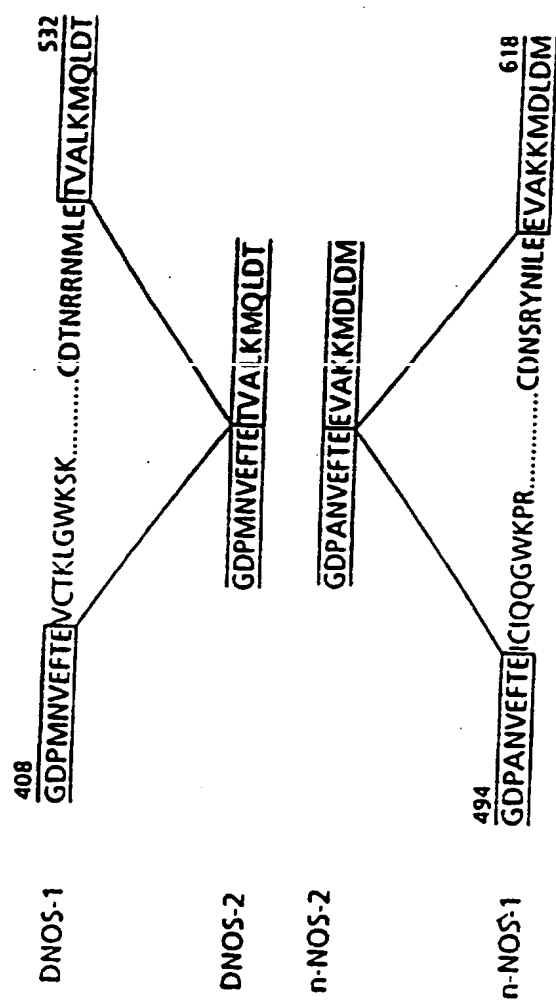


FIGURE 18C

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GGCTTGGAGTACGAGCCGGGTGATCATGTGGGCATCTTTCCGGCGAATCGAACGGA
ACTGGTCGACGGACTGCTAAATCGACTGGTGGGTGTGGATAATCCCGACGAGGTGC
TGCAGTTGCAATTGCTAAAGGAAAAGCAGACATCGAATGGTATATTCAAGTGCTGG
GAGCCGCACGACAAAATACCGCCGGATACTCTAAGGAATCTACTGGCCCCGATTCTTT
GATCTGACCACTCCGCCATCGCGACAGCTACTCACCTGCTGGCTGGATTCTGTGAG
GACACCGCGGACAAGGAGCGGGCTGGAGTTGCTGGTCAACGATTGCTCGGCCTACGA
GGACTGGCGGCACTGGCGGCTGCCGCACCTGCTGGACGTCCTCGAGGAGTTCCCTTC
GTGCCGACCACCGGCTCCCTTCTGCTTGCCCAACTAACGCCGCTGCAGCCTCGCTT
CTATTCATTTCTCGTCGCCGCGCCGCGTTAGTGACGAAATCCACCTGACGGTGGC
CATCGTGAAGTACCGTTGTGAAGATGGTCAGGGTGACGAGCGGTACGGCGTGTGCT
CTAACTATCTATCCGGCTTGCGGGCAGACGACGAGCTGTTTCATGTTGCTGAGAAGCG
CCTTGGGCTTCCATTTGCCCAGCGATCGGAGTCGTCCCATTAATTCTGATTGGTCTCTGG
CACAGGAATAGCTCCATTCCGCTCCTTTGGCAGGAGTTCAGGTGCTACGCGACCT
TGATCCACGGCCAAATTGCCCAAGATGTGGCTCTTCTTTGGCTGCCGGAATCGGGA
TGTTGGACTTGTACGCCGAGGAGAAGGCAGAGCTACAGAAGGATCAAATCCTAGACC
GAGTTTTTCTCGCTCTGTCCAGGGAGCAGGCCATTCCGAAGACATATGTGCAGGACC
TGATTGAGCAGGAATTCGATTCTGTTGTACCAAGTTGATTGTCCAGGAGCGGGGCCACA
TCTACGTCTGCGGCGATGTCACAAATGGCCGAGCATGTGTACCAGACCATCAGGAAGT
GCATTGCCGGCAAAGAGCAGAAAAGCGAGGCGGAAGTTGAGACATTTTTGCTAACA
CTGCGGGACGAAAGTCGCTACCACGAGGACATCTTTGGCATCACGCTGCGAACGGC
TGAGATACACAAAAGTCAAGGGCCACGGCCAGGATACGAATGGCCTCCCAGCCCT
AAGGATAGATATTCGAAGTAATCAAAATAGGAGGGTGACATATCCAAATTCGAGAG
GAATACCAAGCACTTGCTCTTTTTTTCTTCCATATTCAAATGCAATTAATATTGTC
GCTTTGTTTATTACATATTCTGATGAATAACGTTTAAATAAATTACATTTTATTATTG
ATTCTAATGTACAAATCAATTGTGAAATCAAAATCTAAATGTAAATATATTTCAA
ATAAACGAATCGAAAAGGAATTC

FIGURE 19B

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/13198

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C12N15/53 C07K14/435 C12N9/02 A61K38/17
A61K38/44 G01N33/68 //A01K67/027, C07K16/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C07K C12N G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DNA AND CELL BIOLOGY, (1993 SEP) 12 (7) 589-95, USUI, T. ET AL. 'Isolation of Drosophila CREB -B: a novel CRE-binding protein.'	26,27
A	see the whole document ---	18-28
X	MOLECULAR AND CELLULAR BIOLOGY, (1992 SEP) 12 (9) 4123-31, SMOLIK, S. ET AL. 'A cyclic AMP-responsive element-binding transcriptional activator in Drosophila melanogaster, dCREB-A, is a member of the leucine zipper family.' see the whole document ---	29
	-/--	

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

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- *A* document member of the same patent family

Date of the actual completion of the international search

21 March 1996

Date of mailing of the international search report

26.03.96

Name and mailing address of the ISA

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Authorized officer

Andres, S

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
O,X	23RD ANNUAL MEETING OF THE SOCIETY FOR NEUROSCIENCE, WASHINGTON, D.C., USA, NOVEMBER 7-12, 1993. SOCIETY FOR NEUROSCIENCE ABSTRACTS 19-(1-3). 1993. 1066, XP 000566270 TULLY, T. ET AL. 'Independent memories in Drosophila after Pavlovian conditioning.' see abstract	36
A	--- MOLECULAR ENDOCRINOLOGY, vol. 7, no. 2, February 1993 page 145-153 DE GROOT, R. & SASSONE-CORSI, P. 'Hormonal control of gene expression: multiplicity and versatility of cyclic adenosine 3',5'-monophosphate-responsive nuclear regulators' cited in the application see figure 3	1-28
A	--- EUROPEAN JOURNAL OF NEUROSCIENCE, (1994 AUG 1) 6 (8) 1362-70, MULLER, U. 'Ca ²⁺ /calmodulin-dependent nitric oxide synthase in Apis mellifera and Drosophila melanogaster.' see the whole document	33-35
A	--- SCIENCE, vol. 265, 22 July 1994 US, pages 542-546, O'DELL, T. ET AL. 'endothelial NOS and the blockage of LTP by NOS inhibitors in mice lacking neuronal NOS' cited in the application see the whole document	33-36
A	--- EMBO JOURNAL, vol. 11, 1992 EYNSHAM, OXFORD GB, pages 1503-1512, RUPPERT, S. ET AL. 'Multiple mRNA isoforms of the transcription activator protein CREB: generation by alternative splicing and specific expression in primary spermatocytes' cited in the application see figure 3	1,2,6,28
P,X	--- CELL, (1994 OCT 7) 79 (1) 49-58, YIN, J. ET AL. 'Induction of a dominant negative CREB transgene specifically blocks long - term memory in Drosophila.' see the whole document	1-28,36,37
	--- -/--	

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	CELL, (1995 APR 7) 81 (1) 107-15, YIN, J. ET AL. 'CREB as a memory modulator: induced expression of a dCREB2 activator isoform enhances long - term memory in Drosophila.' see the whole document ---	1-28,36, 37
P,X	MOLECULAR AND CELLULAR BIOLOGY, (1995 SEP) 15 (9) 5123-30, YIN, J. ET AL. 'A Drosophila CREB /CREM homolog encodes multiple isoforms, including a cyclic AMP-dependent protein kinase-responsive transcriptional activator and antagonist.' see the whole document ---	1-28
P,X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1995 SEP 26) 92 (20) 9072-6, REGULSKI, M. ET AL. 'Molecular and biochemical characterization of dNOS: a Drosophila Ca ²⁺ /calmodulin-dependent nitric oxide synthase.' see the whole document -----	33-35

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/13198

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 1-9, 11-16
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 1-9, 11-16 are directed to a method of treatment of (diagnostic method practised on) the human/animal body, the search has been carried out and based on the alleged effects of the compound/ composition.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :

C12N 15/12, 15/53, C07K 14/435, C12N
9/02, A61K 38/17, 38/44, G01N 33/68 //
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(11) International Publication Number:

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08/361,063 21 December 1994 (21.12.94) US

(60) Parent Applications or Grants

(63) Related by Continuation

US 08/319,866 (CIP)
Filed on 7 October 1994 (07.10.94)
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Filed on 21 December 1994 (21.12.94)(71) Applicant (for all designated States except US): COLD
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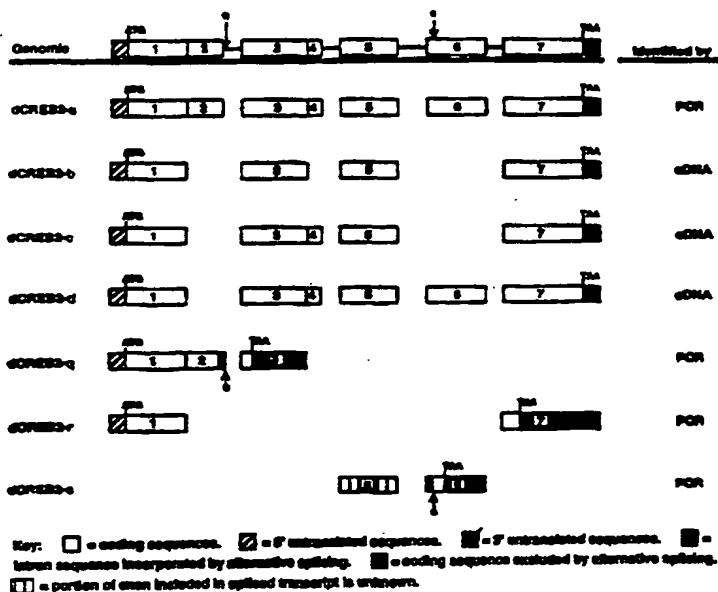
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(US).(74) Agents: GRANAHAAN, Patricia et al.; Hamilton, Brook, Smith
& Reynolds, Two Militia Drive, Lexington, MA 02173
(US).(81) Designated States: CA, JP, MX, US, European patent (AT,
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PT, SE).

Published

With international search report.

Before the expiration of the time limit for amending the
claims and to be republished in the event of the receipt of
amendments.

(54) Title: CLONING AND CHARACTERIZING OF GENES ASSOCIATED WITH LONG-TERM MEMORY



(57) Abstract

A method of regulating long-term memory is disclosed. Also disclosed is isolated DNA encoding a cyclic 3', 5'-adenosine monophosphate responsive transcriptional activator, isolated DNA encoding a' antagonist of cyclic 3', 5'-adenosine monophosphate-inducible transcription, isolated DNA encoding an enhancer-specific activator, and isolated DNA encoding a nitric oxide synthase. A method for assessing the effect of a drug on long-term memory formation is also disclosed.

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CLONING AND CHARACTERIZING OF GENES
ASSOCIATED WITH LONG-TERM MEMORY

Description

Background of the Invention

5 Activation of the cyclic 3',5'-adenosine monophosphate (cAMP) signal transduction pathway can have long-lasting global consequences through its influence on the expression of specific genes. This is true for simple organisms as well as mammals, where many of the known cAMP-responsive
10 genes can have important neural and endocrine roles. Additional information regarding activation of this pathway would be useful, particularly as this activation pertains to the ability of animals to remember activities or events.

Summary of the Invention

15 The present invention is based on Applicants' discovery of the dCREB1 and dCREB2 genes. The present invention is further based on Applicants' discovery that the *Drosophila* CREB2 gene codes for proteins of opposite functions. One isoform (e.g., dCREB2-a) encodes a cyclic
20 3',5'-adenosine monophosphate (cAMP)-responsive transcriptional activator. Another isoform (e.g., dCREB2-b) codes for an antagonist which blocks the activity of the activator.

 When the blocking form is placed under the control of
25 the heat-shock promoter, and transgenic flies are made, a brief shift in temperature induces the synthesis of the blocker in the transgenic fly. This induction of the blocker (also referred to herein as the repressor) specifically disrupts long-term, protein synthesis
30 dependent memory of an odor-avoidance behavioral paradigm.

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As a result of Applicants' discovery, a method is herein provided to regulate long term memory in an animal. The method of regulating long term memory described herein comprises inducing expression of a dCREB2 gene or a
5 fragment thereof in the animal.

The dCREB2 gene encodes several isoforms. Examples of an isoform encoded by the dCREB2 gene are dCREB2-a, dCREB2-b, dCREB2-c, dCREB2-d, dCREB2-q, dCREB2-r and dCREB2-s.

The isoforms encoded by the dCREB2 gene include cAMP-
10 responsive activator isoforms and antagonistic blocker (or repressor) isoforms of the activator isoforms. Cyclic AMP responsive activator isoforms can function as a cAMP-responsive activator of transcription. Antagonistic repressors can act as a blocker of activators. An example
15 of a cAMP-responsive activator isoform is dCREB2-a. An example of an antagonistic repressor (or blocker) isoform is dCREB2-b. The terms blocker and repressor are used interchangeably herein.

In one embodiment of the invention, the dCREB-2 gene
20 encodes a cAMP-responsive activator isoform and inducing said gene results in the potentiation of long term memory.

Alternatively, inducing the dCREB2 gene encoding a cAMP-responsive activator isoform activates the production of a protein which is necessary for the formation of long
25 term memory.

In another embodiment of the invention, the dCREB2 gene encodes a repressor isoform and inducing said gene results in the blocking of long term memory.

A further embodiment of the invention relates to a
30 method of regulating long term memory in an animal comprising inducing repressor and activator isoforms of dCREB2 wherein long term memory is potentiated in the animal when the net amount of functional activator (ΔC) is greater than zero.

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The invention also relates to a method of identifying a substance capable of affecting long term memory in an animal comprising the determination that said substance alters the induction or activity of repressor and activator isoforms of dCREB2 from normal in the animal.

As referred to herein, an activator isoform includes dCREB2-a and functional fragments thereof and a repressor isoform includes dCREB2-b and functional fragments thereof.

Other embodiments of the invention relate to a method of enhancing long term memory formation in an animal comprising increasing the level of activator homodimer from normal, decreasing the level of activator-repressor heterodimer from normal, or decreasing the level of repressor homodimer from normal in the animal.

Still another embodiment of the invention relates to a method of identifying a substance capable of affecting long term memory in an animal comprising the determination that said substance alters activator homodimer, activator-repressor heterodimer and/or repressor homodimer formation from normal in the animal.

As referred to herein, an activator homodimer includes the dCREB2a homodimer, an activator-repressor heterodimer includes the dCREB2a-dCREB2b heterodimer, and a repressor homodimer includes the dCREB2b homodimer.

A further embodiment of the invention relates to isolated DNA encoding a cAMP responsive transcriptional activator. Such a cAMP responsive transcriptional activator can be encoded by a *Drosophila* dCREB2 gene or by homologues or functional fragments thereof. For example, a cAMP responsive transcriptional activator can be encoded by the dCREB2 gene which codes for dCREB2-a or by a gene encoded by the sequences presented herein.

Still another embodiment of the invention relates to isolated DNA encoding an antagonist of cAMP-inducible transcription. Such an antagonist of cAMP-inducible

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transcription can be encoded by a *Drosophila* dCREB2 gene or by homologues or functional fragments thereof. For example, an antagonist of cAMP-inducible transcription can be encoded by the dCREB2 gene which codes for dCREB2-b.

5 Another embodiment of the invention relates to isolated DNA (SEQ ID NO.: 25) which encodes a *Drosophila* dCREB2 gene or functional fragments thereof.

A further embodiment of the invention relates to isolated DNA encoding an enhancer-specific activator. Such
10 an enhancer-specific activator can be encoded by a *Drosophila* dCREB1 gene or by homologues or functional fragments thereof.

Another embodiment of the invention relates to isolated DNA encoding a nitric oxide synthase of *Drosophila*
15 (DNOS). Such DNA can encode a DNOS of neuronal locus. The DNOS encoded can contain, for example, putative heme, calmodulin, flavin mononucleotide (FMN), flavin adenine dinucleotide (FAD) and nicotinamide adenine dinucleotide phosphate, in its reduced form, (NADPH) binding site
20 domains.

A further embodiment of the invention relates to a method for assessing the effect of a drug on long term memory formation comprising administering the drug to *Drosophila*, subjecting the *Drosophila* to classical
25 conditioning to at least one odorant and electrical shock, and assessing the performance index of the classical conditioning, wherein the effect of the drug occurs when it alters the performance index from normal. The drug can affect long term memory formation by, for example, altering
30 the induction or activity of repressor and activator isoforms of dCREB2.

A still further embodiment of the invention relates to the assessment that an animal will have an enhanced or, alternatively, a diminished capability of possessing long
35 term memory. This assessment can be performed by

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determining the amount of cAMP-responsive activator isoforms, cAMP-responsive repressor or blocker isoforms, or dimers of these isoforms that are present in the animal, where these isoforms are encoded by the CREB2 or a homologous gene. Enhanced capability of possessing long term memory will be more likely as the amount of activator exceeds the amount of repressor, i.e. in direct proportion to the size of the net amount of functional activator (ΔC) when this quantity is greater than zero. Conversely, diminished capability of processing long term memory will be more likely as the amount of repressor exceeds the amount of activator, i.e. in direct proportion to the size of the net amount of functional activator (ΔC) when this quantity is less than zero.

Another embodiment of the invention relates to a screening assay of pharmaceutical agents as enhancers of long term memory or as obstructors of long term memory in animals. The screening assay is performed by determining the change in the amount of cAMP-responsive activator isoforms, cAMP-responsive repressor or blocker isoforms, or dimers of these isoforms that is present in an animal or, more preferably, in a cell culture system or in *Drosophila* when the pharmaceutical agent is present, in comparison to when the pharmaceutical agent is not present, where these isoforms are encoded by the CREB2 or a homologous gene. Enhancers of long term memory cause a net increase in the amount of activator isoforms relative to the amount of repressor isoforms, i.e. an increase in the net amount of functional activator (ΔC). Obstructors of long term memory cause a net decrease in the amount of activator isoforms relative to the amount of repressor isoforms, i.e. a decrease in the net amount of functional activator (ΔC). The pharmaceutical agent can cause these changes by acting, for example, to alter the expression (transcription or translation) of the respective activator and/or repressor

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isoforms from the CREB2 or a homologous gene, to alter the formation of activator homodimers, activator-repressor heterodimers and/or repressor homodimers from the expressed isoforms, or to alter the interaction of one or more of these isoform or dimer types at their molecular targets. The long term memory activator isoform/repressor isoform system herein disclosed provides a unique platform for conducting such screening assays.

A further embodiment of the invention relates to an assay of pharmaceutical agents for their property as facilitators or hinderers of long term memory in animals. The assay is performed by administering the pharmaceutical agent to *Drosophila* prior to subjecting the *Drosophila* to a Pavlovian olfactory learning regimen. This regimen assesses the long term memory capabilities of the *Drosophila* by subjecting the flies to a massed and/or a spaced training schedule. Transgenic lines of these flies containing altered dCREB2 genes can be used to further elucidate the long term memory facilitation or hindering property of the pharmaceutical agent. The assay provides data regarding the acquisition of long term memory by the *Drosophila* after exposure to the pharmaceutical agent. These data are compared to long term memory acquisition data from *Drosophila* that have not been exposed to the pharmaceutical agent. If the exposed flies display faster or better retained long term memory acquisition than the unexposed flies, the pharmaceutical agent can be considered to be a facilitator of long term memory. Conversely, if the exposed flies display slower or less retained long term memory acquisition than the unexposed flies, the pharmaceutical agent can be considered to be a hinderer of long term memory. Since the genetic locus for this long term memory assay in *Drosophila* resides in the dCREB2 gene, the results from this assay can be directly applied to

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other animals that have homologous genetic loci (CREB2 or CREM genes).

Brief Description of the Drawings

Figure 1A depicts the DNA sequence (SEQ ID NO.: 1) and predicted amino acid sequence (SEQ ID NO.: 2) of the *dCREB2-a* coding region. The basic region and leucine zipper domains are indicated by solid and broken bold underlining, respectively; positively-charged residues in the basic region are circled; periodic leucines in the zipper motif are boxed; glutamines in the activation domain are underlined; the short amino acid motif with target sites for kinases, starting at residue 227, is indicated by a bold outline; and sequences specified by alternatively-spliced exons 2, 4 and 6 are shaded.

Figure 1B depicts the amino acid sequences of the bZIP domains of *dCREB2* (SEQ ID NO.: 3), mammalian CREB (SEQ ID NO.: 4), CREM (SEQ ID NO.: 5) and ATF-1 (SEQ ID NO.: 6). Differences between *dCREB2* and CREB are boxed.

Figure 2 is a schematic diagram of *dCREB2* isoforms with the exon boundaries defined with respect to *dCREB2-a*. Diagram is not drawn to scale.

Figure 3 is a bar graph representation of results showing pKA-responsive transcriptional activation by *dCREB2-a*.

Figure 4 is a bar graph representation of results showing the transcriptional effect of *dCREB2-b* and a mutant variant on pKA-responsive activation by *dCREB2-a*.

Figure 5 depicts the DNA sequence (SEQ ID NO.: 7) and predicted amino acid sequence (SEQ ID NO.: 8) of the *dCREB1* coding region. The basic region and leucine zipper domains are indicated by solid and broken bold underlining, respectively; positively-charged residues in the basic region are circled; periodic leucines of the zipper motif are boxed; and in the acid-rich region of the activation

domain, negatively-charged amino acids are underlined and proline residues are indicated by diamonds.

Figure 6 is a bar graph representation of results showing transcriptional activation of a CRE reporter gene by *dCREB1* in *Drosophila* Schneider L2 cell culture.

Figure 7A is a photomicrograph of a Northern blot depicting the effect of heat shock induction on *dCREB2-b* expression: wt = wildtype flies; CREB = 17-2 transgenic flies; lanes 1-2: no heat shock; lanes 2-3: immediately after heat shock; lanes 5-6: three hours after heat shock.

Figure 7B is a photograph of a Western blot depicting the effect of heat shock induction on *dCREB2-b* protein production: wt = wildtype flies; CREB = 17-2 transgenic flies; lanes 1-2: no heat shock; lanes 2-3: immediately after heat shock; lanes 5-6: one hour after heat shock; lanes 7-8: three hours after heat shock; lanes 9-10: 9 hours after heat shock; lanes 11-12: 24 hours after heat shock.

Figure 7C is a photograph of a Western blot depicting the effect of heat shock induction on *dCREB2* and *dCREB2-mLZ* (a mutated *dCREB2-b*) protein production: wt = 17-2 transgenic flies (expressing wildtype blocker, *dCREB2-b*); m = A2-2 transgenic flies (expressing mutant blocker, *dCREB2-mLZ*); lanes 1-2: no heat shock; lanes 3-4: immediately after heat shock; lanes 5-6: three hours after heat shock; lanes 7-8: six hours after heat shock.

Figure 8 is a bar graph representation of results showing the effect of cycloheximide (CXM) feeding, before or after spaced or massed training, on one-day memory retention: stripped bars = +CXM; hatched bars = -CXM.

Figure 9A is a bar graph representation of results showing the effect of heat shock induction on one-day memory retention in wildtype (Can-S) flies and *hs-dCREB2-b* transgenic (17-2) flies given spaced or massed training:

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hatched bars = wildtype (Can-S) flies; stripped bars: *hs-dCREB2-b* transgenic (17-2) flies; hs = heat shock.

Figure 9B is a bar graph representation of results showing the effect of heat shock induction on one-day
5 memory retention in wildtype (Can-S) flies or *hs-dCREB2-b* transgenic (M11-1) flies given spaced or massed training: hatched bars = wildtype (Can-S) flies; stripped bars: *hs-dCREB2-b* transgenic (M11-1) flies; hs = heat shock.

Figure 9C is a bar graph representation of results
10 showing the effect of heat shock induction on learning in wildtype (Can-S) flies and *hs-dCREB2-b* transgenic (17-2) flies given spaced or massed training: hatched bars = wildtype (Can-S) flies; stripped bars: *hs-dCREB2-b* transgenic (17-2) flies; hs = heat shock.

Figure 10 is a bar graph representation of results
15 showing the effect of heat shock induction on one-day memory retention in wildtype [*w(isoCJ1)*] flies, *hs-dCREB2-b* transgenic (17-2) flies, and mutant *hs-dCREB2-mLZ* transgenic (A2-2) flies given spaced training: hatched bars
20 = wildtype [*w(isoCJ1)*] flies; stripped bars = *hs-dCREB2-b* transgenic (17-2) flies; white bars = mutant *hs-dCREB2-mLZ* transgenic (A2-2) flies; hs = heat shock.

Figure 11 is a bar graph representation of results showing the effect of heat shock induction on seven-day
25 memory retention (long term memory) in wildtype (Can-S) flies and *hs-dCREB2-b* transgenic (17-2) flies given spaced training: hatched bars = wildtype (Can-S) flies; stripped bars = *hs-dCREB2-b* transgenic (17-2) flies; hs = heat shock.

Figure 12 is a bar graph representation of results showing the effect of heat shock induction on one-day
30 memory retention in *hs-dCREB2-b* transgenic (17-2) flies, radish mutant flies, and radish *hs-dCREB2-b* double mutant (*rsh;17-2*) flies given spaced training: hs = heat shock;
35 hatched bars = -hs; stripped bars = +hs.

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Figure 13A is a graphic representation of results showing the effect of repeated training sessions on seven-day memory retention (long term memory) in wildtype (Can-S) flies with long term memory as a function of the number of training sessions indicated by open circles and a negative accelerating exponential Gompertz (growth) function fit to the individual performance indexes (PIs) using a nonlinear iterative least squares method indicated by the solid line.

Figure 13B is a graphic representation of results showing the effect of the rest interval between each training session on seven-day memory retention (long term memory) in wildtype (Can-S) flies with long term memory as a function of the rest interval indicated by open circles and a negative accelerating exponential Gompertz (growth) function fit to the individual performance indexes (PIs) using a nonlinear iterative least squares method indicated by the solid line.

Figure 14 depicts a conceptual model of a molecular switch for the formation of long term memory based on differential regulation of CREB isoforms with opposing functions with ΔC indicating the net effect of CREB activators.

Figure 15A is a bar graph representation of results showing the effect of 48 massed training sessions (48x massed) or 10 spaced training sessions with a 15-minute rest interval (10x spaced) on seven-day memory retention in wildtype (Can-S) flies.

Figure 15B is a bar graph representation of results showing the effect of one (1x), two (2x) or ten (10x) massed training sessions, three hours after heat-shock induction of the transgene (induced) or in the absence of heat-shock (uninduced), on seven-day memory retention in wildtype (Can-S) flies, *hsp-dCREB2-a* transgenic (C28) flies, and *hsp-dCREB2-a* transgenic (C30) flies: black bars = wildtype (Can-S) flies; stripped bars = *hsp-dCREB2-a*

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transgenic (C28) flies; and white bars = *hsp-dCREB2-a* transgenic (C30) flies.

Figure 15C is a bar graph representation of results showing responses three hours after heat shock in wildtype
5 (Can-S) flies and *hsp-dCREB2-a* transgenic (C28) flies to odors, either octanol (OCT) or methylcyclohexanol (MCH), or to shock (60 V DC): black bars = wildtype (Can-S) flies; stripped bars = *hsp-dCREB2-a* transgenic (C28) flies.

Figure 16A-16C depict the deduced amino acid sequences
10 of DNOS and mammalian NOSs with amino acid numbering starting at the first methionine in each open reading frame (ORF), putative binding domains for cofactors (overlined) demarcated as in previously published reports on mammalian NOSs, and amino acids which have been proposed as contacts
15 with FAD and NADPH based on crystal structure of the ferredoxin NADP⁺ reductase (Karpplus, P. A., *Science*, 251: 60-66 (1991)) conserved at equivalent positions (bullet points): DNOS, *Drosophila* NOS (SEQ ID NO.: 9); RNNOS, rat neuronal NOS (SEQ ID NO.: 10); BENOS, bovine endothelial
20 NOS (SEQ ID NO.: 11); MMNOS, mouse macrophage NOS (SEQ ID NO.: 12). Sequence alignment and secondary structure predictions were performed by Geneworks 2.3 (IntelliGenetics).

Figure 16D is a schematic diagram of the domain
25 structure of *Drosophila* and mammalian NOS proteins with the proposed cofactor-binding sites for heme (H), calmodulin (CaM), flavin mononucleotide (FMN), flavin adenine dinucleotide (FAD), nicotinamide adenine dinucleotide phosphate (NADPH) and the glutamine-rich domain (Q) in DNOS
30 shown.

Figure 17A is a photograph of a Western blot showing DNOS expression in 293 human embryonic kidney cells.

Figure 17B is a bar graph representation of results showing DNOS enzyme activity measured in 293 human
35 embryonic kidney cell extracts by conversion of ³H-L-

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arginine to ^3H -L-citrulline: in the presence of exogenous Ca^{2+} or calmodulin (group B); in the presence of 1 mM EGTA without exogenous Ca^{2+} or calmodulin (group C); in the presence of 100 mM L-NAME with exogenous Ca^{2+} or calmodulin (group D).

Figure 18A is a photomicrograph of a Northern blot showing a 5.0 kb dNOS transcript present in *Drosophila* heads: H = head; B = body.

Figure 18B is a photograph of an agarose gel stained with ethidium bromide showing the expression by the dNOS gene of two alternatively spliced mRNA species with the arrows indicating the positions of the DNA fragments of the expected sizes: the 444 bp long-form fragment and the 129 bp short-form fragment. The other bands present in the lane are artifacts from heteroduplexes that failed to denature. KB = size markers.

Figure 18C depicts the alignment of the deduced amino acid sequence of two protein isoforms of DNOS and mouse neuronal NOS: top part shows the relation between two conceptual *Drosophila* NOS proteins, DNOS-1 (amino acid residues 408-427 and 513-532 of SEQ ID NO.: 9) and DNOS-2 (SEQ ID NO.: 14), corresponding to the longer and shorter RT-PCR products, respectively; the bottom part shows the relationship between the relevant regions of two protein isoforms of the mouse neuronal NOS, n-NOS-1 (amino acid residues 494-513 and 599-618; SEQ ID NO.: 13 and SEQ ID NO.: 15, respectively) and n-NOS-2 (SEQ ID NO.: 16); and the numbers indicate the positions of the amino acid residues relative to the first methionine in the respective OFRs.

Figure 19A-19B depicts the nucleotide sequence (SEQ ID NO.: 25) of a dNOS cDNA encoding the DNOS protein. The open reading frame of 4050 bp starts at nucleotide 189 and ends at nucleotide 4248.

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Detailed Description of the Invention

Applicants have cloned and characterized two genes, designated *dCREB2* and *dCREB1*, isolated through a DNA-binding expression screen of a *Drosophila* head cDNA library in which a probe containing three cAMP-responsive element (CRE) sites was used.

The *dCREB2* gene codes for the first known cAMP-dependent protein kinase (PKA) responsive CREB/ATF transcriptional activator in *Drosophila*. A protein data base search showed mammalian CREB, CREM and ATF-1 gene products as homologous to *dCREB2*. For these reasons, *dCREB2* is considered to be a member, not only of the CREB/ATF family, but of the specific cAMP-responsive CREB/CREM/ATF-1 subfamily. It is reasonable to expect that *dCREB2* is involved in *Drosophila* processes which are analogous to those which are thought to depend on cAMP-responsive transcriptional activation in other animal systems.

Applicants have shown that the *dCREB2* transcript undergoes alternative splicing. Splice products of *dCREB2* were found to fall into two broad categories: one class of transcripts (*dCREB2-a*, *-b*, *-c*, *-d*) which employs alternative splicing of exons 2, 4 and 6 to produce isoforms whose protein products all have the bZIP domains attached to different versions of the activation domain and a second class of transcripts (*dCREB2-q*, *-r*, *-s*) which have splice sites which result in in-frame stop codons at various positions upstream of the bZIP domain. These all predict truncated activation domains without dimerization or DNA binary activity.

dCREB2-a, *-b*, *-c* and *-d* are splice forms that predict variants of the activation domain attached to a common basic region-leucine zipper. These alternative splice forms result in seemingly minor changes in the size and spacing of parts of the activation domain. Nevertheless,

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alternative splicing of the activation domain has profound effects on the functional properties of dCREB2 products. Isoform dCREB2-a produces a PKA-responsive transcriptional activator in cell culture, whereas dCREB2-b, lacking exons
5 2 and 6, produces a specific antagonist. This dCREB2 splicing pattern (and its functional consequences) is virtually identical to that seen in the CREM gene. Similarly located, alternatively-spliced exons in the CREM gene determine whether a particular isoform is an activator
10 or an antagonist (deGroot, R.P. and P. Sassone-Corsi, *Mol. Endocrinol.*, 7: 145-153 (1993); Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)).

The ability of the phosphorylation domain (KID domain) to activate *in trans* other constitutive transcription
15 factors which are bound nearby could potentially transform a CREM antagonist (which contains the KID domain but is lacking an exon needed for activation) into a cAMP-responsive activator. Since the modular organization of these molecules has been conserved, dCREB2-d could have
20 this property.

In contrast to the dCREB2 splicing variants that encode isoforms with a basic region-leucine zipper domain, the dCREB2-q, -r and -s splice forms incorporate in-frame stop codons whose predicted protein products are truncated
25 before the bZIP region. Isoforms of this type have been identified among the products of the CREB gene (deGroot, R.P. and P. Sassone-Corsi, *Mol. Endocrinol.*, 7: 145-153 (1993); Ruppert, S. et al., *EMBO J.*, 11: 1503-1512 (1992)) but not the CREM gene. The function of these truncated
30 CREB molecules is not known, but at least one such CREB mRNA is cyclically regulated in rat spermatogenesis (Waeber, G. et al., *Mol. Endocrinol.*, 5: 1418-1430 (1991)).

So far, dCREB2 is the only cAMP-responsive CREB transcription factor isolated from *Drosophila*. Other
35 *Drosophila* CREB molecules, BBF-2/dCREB-A (Abel, T. et al.,

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Genes Dev., 6: 466-488 (1992); Smolik, S.M. et al., *Mol. Cell Biol.*, 12: 4123-4131 (1992)), *dCREB-B* (Usui, T. et al., *DNA and Cell Biology*, 12(7): 589-595 (1993)) and *dCREB1*, have less homology to mammalian CREB and CREM. It may be that *dCREB2* subsumes functions of both the CREB and CREM genes in *Drosophila*. The mammalian CREB and CREM genes are remarkably similar to one another in several respects. It has been suggested that CREB and CREM are the product of a gene duplication event (Liu, F. et al., *J. Biol. Chem.*, 268: 6714-6720 (1993); Riabowol, K.T. et al., *Cold Spring Harbor Symp. Quant. Biol.*, 1: 85-90 (1988)). *dCREB2* has a striking degree of amino acid sequence similarity to the CREB and CREM genes in the bZIP domain. Moreover, comparison of alternative splicing patterns among CREB, CREM and *dCREB2* indicates that *dCREB2* generates mRNA splicing isoforms similar to exclusive products of both CREB and CREM. Taken together, the sequence information and the splicing organization suggest that *dCREB2* is an ancestor of both the mammalian CREB and CREM genes.

As discussed further herein, one phenomenon in which *dCREB2* might act with enduring consequences is in long-term memory. This possibility is a particularly tempting one because recent work in *Aplysia* indicates that a CREB factor is likely to function in long-term facilitation by inducing an "immediate early" gene (Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994); Dash, P.K., *Nature*, 345: 718-721 (1990)). Recent experiments with a conditionally-expressed *dCREB2-b* transgene indicate that it has specific effects on long-term memory in *Drosophila*.

The product of the second gene described herein, *dCREB1*, also appears to be a member of the CREB/ATF family. Gel-retardation assays indicate that it binds specifically to CREs. It has a basic region and an adjacent leucine zipper at its carboxyl end, but this domain shows limited amino acid sequence similarity to other CREB/ATF genes.

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The presumed transcriptional activation domain of *dCREB1* is of the acid-rich variety. Furthermore, it has no consensus phosphorylation site for PKA. *dCREB1* can mediate transcriptional activation from CRE-containing reporters in the *Drosophila* L2 cell line, but this activation is not dependent on PKA.

A recurrent finding from work on the biology of learning and memory is the central involvement of the cAMP signal transduction pathway. In *Aplysia*, the cAMP second-messenger system is critically involved in neural events underlying both associative and non-associative modulation of a behavioral reflex (Kandel, E.R. and J.H. Schwartz, *Science*, 218: 433-443 (1982); Kandel, E.R., et al., In *Synaptic Function*, Edelman, G.M., et al. (Eds.), John Wiley and Sons, New York (1987); Byrne, J.H., et al., In *Advances in Second Messenger and Phosphoprotein Research*, Shenolikar, S. and A.C. Nairn (Eds.), Raven Press, New York, pp. 47-107 (1993)). In *Drosophila*, two mutants, *dunce* and *rutabaga*, were isolated in a behavioral screen for defects in associative learning and are lesioned in genes directly involved in cAMP metabolism (Quinn, W.G., et al., *Proc. Natl. Acad. Sci. USA*, 71: 708-712 (1974); Dudai, Y., et al., *Proc. Natl. Acad. Sci., USA* 73: 1684-1688 (1976); Byers, D. et al., *Nature*, 289: 79-81 (1981); Livingstone, M.S., et al., *Cell*, 37: 205-215 (1984); Chen, C.N. et al., *Proc. Natl. Acad. Sci. USA*, 83: 9313-9317 (1986); Levin, L.R., et al., *Cell*, 68: 479-489 (1992)). These latter observations were extended with a reverse-genetic approach using inducible transgenes expressing peptide inhibitors of cAMP-dependent protein kinase (PKA) and with analyses of mutants in the PKA catalytic subunit (Drain, P. et al., *Neuron*, 6: 71-82 (1991); Skoulakis, E.M., et al., *Neuron*, 11: 197-208 (1993)). Recent work on mammalian long-term potentiation (LTP) also has indicated a role for cAMP in synaptic

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plasticity (Frey, U., et al., *Science*, 260: 1661-1664 (1993); Huang, Y.Y. and E.R. Kandel, *In Learning and Memory*, vol. 1, pp.74-82, Cold Spring Harbor Press, Cold Spring Harbor, NY (1994)).

5 The formation of long-lasting memory in animals and of long-term facilitation in *Aplysia* can be disrupted by drugs that interfere with transcription or translation (Agranoff, B.W. et al., *Brain Res.*, 1: 303-309 (1966); Barondes, S.H. and H.D. Cohen, *Nature*, 218: 271-273 (1968); Davis, H.P.
10 and L.R. Squire, *Psychol. Bull.*, 96: 518-559 (1984); Rosenzweig, M.R. and E.L. Bennett, *In Neurobiology of Learning and Memory*, Lynch, G., et al. (Eds.), The Guilford Press, New York, pp. 263-288, (1984); Montarolo, P.G., et al., *Science*, 234: 1249-1254 (1986)). This suggests that
15 memory consolidation requires *de novo* gene expression. Considered along with the involvement of the cAMP second-messenger pathway, this requirement for newly synthesized gene products suggests a role for cAMP-dependent gene expression in long-term memory (LTM)
20 formation.

In mammals, a subset of genes from the CREB/ATF family are known to mediate cAMP-responsive transcription (Habener, J.F., *Mol. Endocrinol.*, 4: 1087-1094 (1990); deGroot, R.P. and P. Sassone-Corsi, *Mol. Endocrinol.*, 7:
25 145-153 (1993)). CREBs are members of the basic region-leucine zipper transcription factor superfamily; (Landschulz, W.H. et al., *Science*, 240: 1759-1764 (1988)). The leucine zipper domain mediates selective homo- and hetero-dimer formation among family members (Hai, T.Y. et
30 al., *Genes & Dev.*, 3: 2083-2090 (1989); Hai, T. and T. Curran, *Proc. Natl. Acad. Sci. USA*, 88: 3720-3724 (1991)). CREB dimers bind to a conserved enhancer element (CRE) found in the upstream control region of many cAMP-responsive mammalian genes (Yamamoto, K.K., et al.,
35 *Nature*, 334: 494-498 (1988)). Some CREBs become

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transcriptional activators when specifically phosphorylated by PKA (Gonzalez, G.A. and M.R. Montminy, *Cell*, 59: 675-680 (1989); Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)), while others, isoforms from the CREM gene, are functional antagonists of these PKA-responsive activators (Foulkes, N.S. et al., *Cell*, 64: 739-749 (1991); Foulkes, N. and P. Sassone-Corsi, *Cell*, 68: 411-414 (1992)).

Work in *Aplysia* has shown that cAMP-responsive transcription is involved in long-term synaptic plasticity (Schacher, S. et al., *Science*, 240: 1667-1669 (1988); Dash, P.K., *Nature*, 345: 718-721 (1990)). A primary neuronal co-culture system has been used to study facilitation of synaptic transmission between sensory and motor neurons comprising the monosynaptic component of the *Aplysia* gill-withdrawal reflex. Injection of oligonucleotides containing CRE sites into the nucleus of the sensory neuron specifically blocked long-term facilitation (Dash, P.K., *Nature*, 345: 718-721 (1990)). This result suggests that titration of CREB activity might disrupt long-term synaptic plasticity.

Described herein is the cloning and characterization of a *Drosophila* CREB gene, dCREB2. This gene produces several isoforms that share overall structural homology and nearly complete amino acid identity in the basic region-leucine zipper with mammalian CREBs. The dCREB2-a isoform is a PKA-responsive transcriptional activator whereas the dCREB2-b product blocks PKA-responsive transcription by dCREB2-a in cell culture. These molecules with opposing activities are similar in function to isoforms of the mammalian CREM gene (Foulkes, N.S. et al., *Cell*, 64: 739-749 (1991); Foulkes, N. and P. Sassone-Corsi, *Cell*, 68: 411-414 (1992); Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)). The numerous similarities in sequence and function between dCREB2 and mammalian CREBs suggest

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that cAMP-responsive transcription is evolutionarily conserved.

Genetic studies of memory formation in *Drosophila* have revealed that the formation of a protein synthesis-
5 dependent long-term memory (LTM) requires multiple training sessions with a rest interval between them. As discussed further herein, this LTM is blocked specifically by induced expression of a repressor isoform of the cAMP-responsive transcription factor CREB. Also as discussed further
10 herein, LTM information is enhanced after induced expression of an activator form of CREB. Maximum LTM is achieved after just one training session.

To investigate the role of CREBs in long-term memory (LTM) formation in *Drosophila*, dominant-negative transgenic
15 lines which express *dCREB2-b* under the control of a heat-shock promoter (*hs-dCREB2-b*) were generated. Groups of flies, which had been heat-shock induced or left uninduced, were tested for memory retention after Pavlovian olfactory learning. This acute induction regimen minimized
20 potential complications from inappropriate expression of *dCREB2-b* during development and allowed a clear assessment of the effect of *hs-dCREB2-b* induction on memory formation.

In *Drosophila*, consolidated memory after olfactory learning is composed of two genetically distinct
25 components: anesthesia-resistant memory (ARM) and long-term memory (LTM). ARM decays to zero within four days after training, and formation of ARM is insensitive to the protein synthesis inhibitor cycloheximide (CHX) but is disrupted by the *radish* mutation (Folkers, E., et al.,
30 *Proc. Natl. Acad. Sci. USA*, 90: 8123-8127 (1993)). In contrast, LTM shows essentially no decay over at least seven days, its formation is cycloheximide-sensitive and it is not disrupted by *radish*. Two different training protocols involving massed and spaced sessions were
35 employed (Ebbinghaus, H., *Über das Gedächtnis*, Dover, New

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York (1885); Baddeley, A.D., *The Psychology of Memory*, Basic Books, New York (1976)) to dissect memory formation. The massed training procedure consists of ten consecutive training cycles with no rest interval between them, while
5 the spaced training protocol consists of the same number of sessions but with a 15-minute rest between each. Their genetic dissection revealed that the massed protocol produced only ARM, while the spaced protocol produced memory retention composed of both ARM and LTM.

10 The behavioral results show that formation of LTM is completely blocked by induced expression of hs-dCREB2-b. This effect is remarkable in its behavioral specificity. ARM, a form of consolidated memory genetically distinguishable from LTM, but co-existing with it one-day
15 after spaced training, was not affected. Learning and peripheral behaviors likewise were normal. Thus, the effect of the induced hs-dCREB2-b transgene is specific to LTM.

Induction of the mutant blocker did not affect LTM.
20 This result, together with the molecular data which showed that induction of the wild-type blocker did not have widespread effects on transcription, suggests that the blocker is reasonably specific at the molecular level when it specifically blocks LTM. The wild-type blocker may
25 disrupt cAMP-dependent transcription in vivo, since it can block cAMP-responsive transcription in cell culture. It is reasonable to infer that dimerization is necessary for blocker function and that the wild-type blocker could interfere with cAMP-responsive transcription either by
30 forming heterodimers with dCREB2-a, the activator, or by forming homodimers and competing for DNA binding with homodimers of dCREB2-a. Thus, activators and repressors may form homodimers or heterodimers. It is reasonable to infer that long term memory is enhanced when the level of
35 activator homodimer is increased from normal and/or when

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the level of activator-repressor heterodimer is decreased from normal and/or when the level of repressor homodimer is decreased from normal. In any case, the molecular target(s) of dCREB2-b are likely to be interesting because
5 of the behavioral specificity of the block of LTM.

In *Drosophila*, consolidation of memory into long-lasting forms is subject to disruption by various agents. A single-gene mutation *radish* and the pharmacological agent CXM were used to show that long-lasting memory in flies is
10 dissectable into two components, a CXM-insensitive ARM, which is disrupted by *radish*, and a CXM-sensitive LTM, which is normal in *radish* mutants. As described herein, CREB-family members are likely to be involved in the CXM-sensitive, LTM branch of memory consolidation. The results
15 described herein, taken together with the showing that long-term memory is dissectable into a CXM-insensitive ARM and a CXM-sensitive LTM, show that only one functional component of consolidated memory after olfactory learning lasts longer than four days, requires *de novo* protein
20 synthesis and involves CREB-family members.

Based on work in *Aplysia*, a model has been proposed to describe the molecular mechanism(s) underlying the transition from short-term, protein synthesis-independent to long-term, protein synthesis-dependent synaptic
25 plasticity (Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994)). The present work in *Drosophila* on long-term memory extends this model to the whole organism. Important molecular aspects of this transition seem to involve migration of the catalytic subunit of PKA into the nucleus
30 (Backsai, B.J. et al., *Science*, 260: 222-226 (1993)) and subsequent phosphorylation and activation of CREB-family members (Dash, P.K., *Nature*, 345: 718-721 (1990); Kaang, B.K., et al., *Neuron*, 10: 427-435 (1993)). In flies, it is likely that the endogenous dCREB2-a isoform is one of these
35 nuclear targets. Activated dCREB2-a molecules then might

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transcribe other target genes, including the immediate early genes--as is apparently the case in *Aplysia*. (Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994)).

It is remarkable that the cAMP signal transduction pathway, including its nuclear components, seem to be required for memory-related functions in each of these species and behavioral tasks. Taken together with cellular analyses of a long-lasting form of LTP in hippocampal slices (Frey, U., et al., *Science*, 260: 1661-1664 (1993); Huang, Y.Y. and E.R. Kandel, *In Learning and Memory*, vol. 1, pp.74-82, Cold Spring Harbor Press, Cold Spring Harbor, NY (1994)), the emerging picture is that cAMP-responsive transcription is a conserved molecular switch involved in the consolidation of short-term memory to long-term memory. Thus, it is reasonable to infer that differential regulation of CREB isoforms serves as a molecular switch for the formation of long term memory.

A universal property of memory formation is that spaced training (repeated training sessions with a rest interval between them) produces stronger, longer-lasting memory than massed training (the same number of training sessions with no rest interval) (Ebbinghaus, H., *Uber das Gedachtnis*, Dover, New York (1885); Hintzman, D.L., *In Theories in Cognitive Psychology: The Loyola Symposium*, R.L. Solso (Ed.), pp. 77-99, Lawrence Erlbaum Assoc., Hillsdale, New Jersey (1974); Carew, T.J., et al., *Science*, 175: 451-454 (1972); Frost, W.N., et al., *Proc. Natl. Acad. Sci. USA*, 82: 8266-8269 (1985)). This phenomenon also exists in fruit flies for a conditioned odor avoidance response (Tully, T. and W.G. Quinn, *J. Comp. Physiol.* 157: 263-277 (1985)). Genetic dissection of this long-lasting memory has revealed, however, an important difference between massed and spaced training. Spaced training produces two functionally independent forms of consolidated

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memory, ARM and LTM, while massed training produces only ARM.

As described herein, ARM and LTM differ primarily in their requirement for protein synthesis during induction.

5 ARM is not affected when flies are fed the protein synthesis inhibitor cycloheximide (CHX) immediately before or after training, while LTM is completely blocked under the same feeding conditions. ARM in normal flies also decays away within four days after training, while LTM

10 shows no decay for at least seven days. Thus, protein synthesis is required to induce LTM, but LTM is maintained indefinitely once formed. These latter properties of LTM have been observed throughout the animal kingdom (Davis, H.P. and L.R. Squire, *Psychol. Bull.*, 96: 518-559 (1984);

15 Castellucci, V.F., et al., *J. Neurobiol.*, 20: 1-9 (1989); Erber, J., *J. Comp. Physiol. Psychol.*, 90: 41-46 (1976); Jaffe, K., *Physiol. Behav.*, 25: 367-371 (1980)). The emerging neurobiological interpretation is that formation of LTM involves protein synthesis-dependent structural

20 changes at relevant synapses (Greenough, W.T., *TINS*, 7: 229-283 (1984); Buonomano, D.V. and J.H. Byrne, *Science*, 249: 420-423 (1990); Nazif, F.A., et al., *Brain Res.*, 539: 324-327 (1991); Stewart, M.G., *In Neural and Behavioural Plasticity: The Use of the Domestic Chick As A Model*, R.J. Andrew (Ed.), pp. 305-328, Oxford, Oxford (1991); Bailey, C.H. and E.R. Kandel, *Sem. Neurosci.*, 6:35-44 (1994)). The modern molecular view is that regulation of gene expression underlies this protein synthesis-dependent effect (Goelet, P. et al., *Nature*, 322: 419-422 (1986); Gall, C.M. and J.C. Lauterborn, *In Memory: Organization and Locus of Change*, L.R. Squire, et al., (Eds.) pp.301-329 (1991); Armstrong, R.C. and M.R. Montminy, *Annu. Rev. Neurosci.*, 16: 17-29 (1993)).

30

Why is spaced training required to induce LTM? The

35 massed and spaced procedures both entail ten training

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sessions; consequently, flies receive equivalent exposure to the relevant stimuli (one odor temporally paired with electric shock and a second odor presented without shock). The only procedural difference between massed and spaced training is the rest interval between each training session. The absence of a rest interval between sessions during massed training does not appear to disrupt the memory formation process. The level of initial learning assayed immediately after massed training is similar to that after spaced training. In addition, ARM levels are similar after both training procedures. Thus, the presence of a rest interval during spaced training seems crucial to the induction of LTM.

To investigate the temporal kinetics of this rest interval in relation to the formation of LTM (Figures 13A and 13B), it was first established that the usual ten sessions of spaced training produced maximal 7-day memory retention (7-day retention is composed solely of LTM, since ARM decays to zero within four days).

Figure 13A shows that 15 or 20 training sessions did not improve memory retention. Thus, ten spaced training sessions produces maximal, asymptotic levels of LTM.

LTM as a function of the length of the rest interval between 10 spaced training sessions was then assessed. Figure 13B reveals a continuous increase in LTM from a 0-min rest interval (massed training) to a 10-minute rest interval, at which time LTM levels reach maximum. Longer rest intervals yielded similar memory scores. These observations of LTM formation suggest an underlying biological process, which changes quantitatively during the rest interval between sessions and which accumulates over repeated training sessions.

In transgenic flies, the formation of LTM, but not ARM or any other aspect of learning or memory, is disrupted by induced expression of a repressor form of the cAMP-

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responsive transcription factor CREB (Example 4). Mutating two amino acids in the "leucine zipper" dimerization domain of this CREB repressor was sufficient to prevent the dominant-negative effect on LTM. Thus, indication of LTM is not only protein synthesis-dependent but also is CREB-dependent. Stated more generally, CREB function is involved specifically in a form of a memory that is induced only by spaced training. This observation was particularly intriguing in light of the molecular nature of CREB.

In *Drosophila*, transcriptional and/or post-translational regulation of dCREB2 yields several mRNA isoforms. Transient transfection assays in mammalian F9 cells have demonstrated that one of these isoforms (CREB2-a) functions as a cAMP-responsive activator of transcription, while a second isoform (CREB2-b) acts as an antagonistic repressor of the activator (Example 1; cf. Habener, J.F., *Mol. Endocrinol.*, 4: 1087-1094 (1990); Foulkes, N. and P. Sassone-Corsi, *Cell*, 68: 411-414 (1992)). (This repressor isoform was used previously to generate the inducible transgene mentioned above.) The existence of different CREB isoforms with opposing functions suggested an explanation for the requirement of multiple training sessions with a rest interval between them for the formation of LTM.

In its simplest form, this model (Example 7; Figure 14) supposes that cAMP-dependent protein kinase (PKA), activated during training, induces the synthesis and/or function of both CREB activator and repressor isoforms (cf. Yamamoto, K.K., et al., *Nature*, 334: 494-498 (1988); Backsai, B.J. et al., *Science*, 260: 222-226 (1993)). Immediately after training, enough CREB repressor exists to block the ability of CREB activator to induce downstream events. Then, CREB repressor isoforms are inactivated faster than CREB activator isoforms. In this manner, the net amount of functional activator ($\Delta C = \text{CREB2a} - \text{CREB2b}$)

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increases during a rest interval and then accumulates over repeated training sessions (with a rest interval) to induce further the downstream targets involved with the formation of LTM (Montarolo, P.G., et al., *Science*, 234: 1249-1254 (1986); Kaang, B.K., et al., *Neuron*, 10: 427-435 (1993)).

This model leads to three predictions, which have been confirmed. First, if the functional difference between CREB activator and repressor isoforms is zero ($\Delta C=0$) immediately after one training session, then additional massed training sessions should never yield LTM. Figure 15A shows that 48 massed training sessions, rather than the usual 10, still does not produce any 7-day memory retention. Second, if the amount of CREB repressor is increased experimentally, ΔC will be negative immediately after training ($\Delta C < 0$). Then, enough CREB repressor may not decay during a rest interval to free enough CREB activator for induction of LTM. This has been shown to be the case for spaced training (15-min rest interval) after inducing the expression of a *hsp-dCREB2-b* (repressor) transgene three hours before training (Example 4). Third, if the amount of CREB activator is increased experimentally, ΔC will be positive immediately after training ($\Delta C > 0$). This effect, then, should eliminate or reduce the rest interval required to induce LTM. Figure 15B shows the results from recent experiments in which the expression of a *hsp-dCREB2-a* (activator) transgene was induced three hours before training. In these transgenic flies, massed training produced maximal LTM. This effect appeared not to arise trivially, since olfactory acuity, shock reactivity (Figure 15C) and initial learning were normal in transgenic flies after heat shock-induction. Thus, the requirement for a rest interval between training sessions to induce LTM specifically was eliminated.

Figure 15B also shows that maximal LTM occurred in induced *hsp-dCREB2-a* transgenic flies after just one

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training session. The usual requirement for additional training to form a strong, long-lasting memory was no longer necessary. Thus, induced overexpression of a CREB activator has produced in otherwise normal flies, the functional equivalent of a "photographic" memory. This result indicates that the amount of CREB activator present during training -- rather than the amount of activated PKA that reaches CREB in the nucleus, for instance (cf. Backsai, B.J. et al., *Science*, 260: 222-226 (1993); Kaang, B.K., et al., *Neuron*, 10: 427-435 (1993); Frank, D.A. and M.E. Greenberg, *Cell*, 79: 5-8 (1994)) -- is the rate-limiting step of LTM formation. Taken together, results from these experiments support the notion that the opposing functions of CREB activators and repressors act as a "molecular switch" (cf. Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)) to determine the parameters of extended training (number of training sessions and rest interval between them) required to form maximum LTM.

To date, seven different dCREB2 RNA isoforms have been identified, and more are hypothesized to exist. Each may be regulated differentially at transcriptional (Meyer, T.E., et al., *Endocrinology*, 132: 770-780 (1993)) and/or translation levels before or during LTM formation. In addition, different combinations of CREB isoforms may exist in different (neuronal) cell types. Consequently, many different combinations of activator and repressor molecules are possible. From this perspective, the notions that all activators and repressors are induced during a training session or that all repressors inactivate faster than activators (see above) need not be true. Instead, the model requires only that ΔC (the net function of activators and repressors) is less than or equal to zero immediately after training and the increases with time (rest interval).

Theoretically, particular combinations of activator and repressor molecules in the relevant neuron(s) should

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determine the rest interval and/or number of training sessions necessary to produce maximum LTM for any particular task or species. Thus, the molecular identification and biochemical characterization of each CREB activator and repressor isoform used during LTM formation in fruit flies is the next major step toward establishing the validity of our proposed model. Similar experiments in other species may establish its generality.

CREB certainly is not involved exclusively with LTM. The *dCREB2* gene, for instance, is expressed in all fruit fly cells and probably acts to regulate several cellular events (Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)).

So, what defines the specificity of its effects on LTM? Specificity most likely resides with the neuronal circuitry involved with a particular learning task. For olfactory learning in fruit flies, for instance, CREB probably is modulated via the cAMP second messenger pathway. Genetic disruptions of other components of this pathway are known to affect olfactory learning and memory (Livingstone, M.S., et al., *Cell*, 37: 205-215 (1984); Drain, P. et al., *Neuron*, 6: 71-82 (1991); Levin, L.R., et al., *Cell*, 68: 479-489 (1992); Skoulakis, E.M., et al., *Neuron* 11: 197-208 (1993); Qiu, Y. and R.L. Davis, *Genes Develop.* 7: 1447-1458 (1993)). Presumably, the stimuli used during conditioning (training) stimulate the underlying neuronal circuits. The cAMP pathway is activated in (some) neurons participating in the circuit, and CREB-dependent regulation of gene expression ensues in the "memory cells". This neurobiological perspective potentially will be established in *Drosophila* by identifying the neurons in which LTM-specific CREB function resides. Experiments using a neuronal co-culture system in *Aplysia* already have contributed significantly to this issue (Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994) and references therein).

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The involvement of CREB in memory, or in the structural changes of neurons which underlie memory in vivo, also has been implicated in mollusks (Dash, P.K., *Nature*, 345: 718-721 (1990); Alberini, C.M. et al., *Cell*, 76: 1099-1114 (1994)) and in mice (Bourtchuladze, R., et al., *Cell*, 79: 59-68 (1994)). Ample evidence also exists for the involvement of the cAMP second messenger pathway in associative learning in *Aplysia* (Kandel, E.R., et al., *In Synaptic Function*, Edelman, G.M., et al. (Eds.), John Wiley and Sons, New York (1987); Byrne, J.H., et al., *In Advances in Second Messenger and Phosphoprotein Research*, Shenolikar, S. and A.C. Nairn (Eds.), Raven Press, New York, pp. 47-107 (1993)) and in rat hippocampal long-term potentiation (LTP), a cellular model of associative learning in vertebrates (Frey, U., et al., *Science*, 260: 1661-1664 (1993); Huang, Y.Y. and E.R. Kandel, *In Learning and Memory*, vol. 1, pp. 74-82, Cold Spring Harbor Press, Cold Spring Harbor, NY (1994)). Finally, cellular and biochemical experiments have suggested that CREB function may be modulated by other second messenger pathways (Dash, P.K., et al., *Proc. Natl. Acad. Sci. USA* 88: 5061-5065 (1991); Ginty, D.D. et al., *Science*, 260: 238-241 (1993); deGroot, R.P. and P. Sassone-Corsi, *Mol. Endocrinol.*, 7: 145-153 (1993)). These observations suggest that CREB might act as a molecular switch for LTM in many species and tasks.

Finally, why might the formation of LTM require a molecular switch? Many associative events occur only once in an animal's lifetime. Forming long-term memories of such events would be unnecessary and if not counterproductive. Instead, discrete events experienced repeatedly are worth remembering. In essence, a recurring event comprises a relevant signal above the noise of one-time events. Teleologically, then, the molecular switch may act as an information filter to ensure that only discrete but

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recurring events are remembered. Such a mechanism would serve efficiently to tailor an individual's behavioral repertoire to its unique environment.

The present invention also relates to isolated DNA
5 having sequences which encode (1) a cyclic 3',5'-adenosine monophosphate (cAMP) responsive transcriptional activator, or a functional fragment thereof, or (2) an antagonist of a cAMP responsive transcriptional activator, or a functional fragment thereof, or (3) both an activator and an
10 antagonist, or functional fragments thereof of both.

The invention relates to isolated DNA having sequences which encode *Drosophila* dCREB2 isoforms, or functional analogues of a dCREB2 isoform. As referred to herein, a functional analogue of a dCREB2 isoform comprises at least
15 one function characteristic of a *Drosophila* dCREB2 isoform, such as a cAMP-responsive transcriptional activator function and/or an antagonistic repressor of the cAMP activator function. These functions (i.e., the capacity to mediate PKA-responsive transcription) may be detected by
20 standard assays (e.g., assays which monitor for CREB-dependent activation). For example, assays in F9 cells have been used extensively to study CREB-dependent activation because their endogenous cAMP-responsive system is inactive; (Gonzalez, G.A. et al., *Nature*, 337: 749-752
25 (1989); Masson, N. et al., *Mol. Cell Biol.*, 12: 1096-1106 (1992); Masson, N. et al., *Nucleic Acids Res.*, 21: 1163-1169 (1993)).

The invention further relates to isolated DNA having sequences which encode a *Drosophila* dCREB2 gene or a
30 functional fragment thereof. Isolated DNA meeting these criteria comprise nucleic acids having sequences identical to sequences of naturally occurring *Drosophila* dCREB2 and portions thereof, or variants of the naturally occurring sequences. Such variants include mutants differing by the

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addition, deletion or substitution of one or more nucleic acids.

The invention relates to isolated DNA that are characterized by (1) their ability to hybridize to a
5 nucleic acid having the DNA sequence in Figure 1A (SEQ ID NO.: 1) or its complement, or (2) by their ability to encode a polypeptide of the amino acid sequence in Figure 1A (SEQ ID NO.: 2) or functional equivalents thereof (i.e., a polypeptide which functions as a cAMP responsive
10 transcriptional activator), or (3) by both characteristics. Isolated nucleic acids meeting these criteria comprise nucleic acids having sequences homologous to sequences of mammalian CREB, CREM and ATF-1 gene products. Isolated nucleic acids meeting these criteria also comprise nucleic
15 acids having sequences identical to sequences of naturally occurring dCREB2 or portions thereof, or variants of the naturally occurring sequences. Such variants include mutants differing by the addition, deletion or substitution of one or more residues, modified nucleic acids in which
20 one or more residues is modified (e.g., DNA or RNA analogs), and mutants comprising one or more modified residues.

Such nucleic acids can be detected and isolated under high stringency conditions or moderate stringency
25 conditions, for example. "High stringency conditions" and "moderate stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 (see particularly 2.10.8-11) and pages 6.3.1-6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. et al., eds,
30 Vol. 1, Suppl. 26, 1991), the teachings of which are incorporated herein by reference. Factors such as probe length, base composition, percent mismatch between the hybridizing sequences, temperature and ionic strength influence the stability of nucleic acid hybrids. Thus,
35 high or moderate stringency conditions can be determined

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empirically, depending in part upon the characteristics of the known DNA to which other unknown nucleic acids are being compared for homology.

Isolated nucleic acids that are characterized by their
5 ability to hybridize to a nucleic acid having the sequence in Figure 1A or its complement (e.g., under high or moderate stringency conditions) may further encode a protein or polypeptide which functions as a CAMP responsive transcriptional activator.

10 The present invention also relates to isolated DNA having sequences which encode an enhancer-specific activator, or a functional fragment thereof.

The invention further relates to isolated DNA having sequences which encode a *Drosophila* dCREB1 gene or a
15 functional fragment thereof. Isolated DNA meeting these criteria comprise nucleic acids having sequences identical to sequences of naturally occurring *Drosophila* dCREB1 and portions thereof, or variants of the naturally occurring sequences. Such variants include mutants differing by the
20 addition, deletion or substitution of one or more nucleic acids.

The invention further relates to isolated DNA that are characterized by (1) their ability to hybridize to a nucleic acid having the DNA sequence in Figure 5 (SEQ ID
25 NO.: 7) or its complement, or (2) by their ability to encode a polypeptide of the amino acid sequence in Figure 5 (SEQ ID NO.: 8), or by both characteristics. Isolated DNA meeting these criteria also comprise nucleic acids having sequences identical to sequences of naturally occurring
30 dCREB1 or portions thereof, or variants of the naturally occurring sequences. Such variants include mutants differing by the addition, deletion or substitution of one or more residues, modified nucleic acids in which one or more residues is modified (e.g., DNA or RNA analogs), and
35 mutants comprising one or more modified residues.

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Such nucleic acids can be detected and isolated under high stringency conditions or moderate stringency conditions as described above, for example.

Fragments of the isolated DNA which code for
5 polypeptides having a certain function can be identified and isolated by, for example, the method of Jasin, M., et al., U.S. Patent No. 4,952,501.

Nitric Oxide in Invertebrates: *Drosophila* dNOS Gene Codes for a Ca^{2+} /Calmodulin-Dependent Nitric Oxide Synthase

10 Nitric oxide (NO) is a gaseous mediator of a wide variety of biological processes in mammalian organisms. Applicants have cloned the *Drosophila* gene, dNOS, coding for a Ca^{2+} /calmodulin-dependent nitric oxide synthase (NOS). Presence of a functional NOS gene in *Drosophila*
15 provides conclusive evidence that invertebrates synthesize NO and presumably use it as a messenger molecule. Furthermore, conservation of an alternative RNA splicing pattern between dNOS and vertebrate neuronal NOS, suggests broader functional homology in biochemistry and/or
20 regulation of NOS.

NO is synthesized by nitric oxide synthases (NOSs) during conversion of L-arginine to L-citrulline (Knowels, R.G., et al., *Biochem. J.*, 298: 249 (1994); Nathan, C., et al., *J. Biol. Chem.*, 269: 13725 (1994); Marletta, M.A., *J. Biol. Chem.*, 268: 12231 (1993)). Biochemical
25 characterization of NOSs has distinguished two general classes: (i) constitutive, dependent on exogenous Ca^{2+} and calmodulin and (ii) inducible, independent of exogenous Ca^{2+} and calmodulin. Analyses of cDNA clones have
30 identified at least three distinct NOS genes in mammals (Bredt, D.S., et al., *Nature*, 351: 714-718 (1991); Lamas, S., et al., *Proc. Natl. Acad. Sci. USA*, 89: 6348-6352 (1992); Lyons, C.R., et al., *J. Biol. Chem.*, 267: 6370 (1992); Lowenstein, C.J., et al., *Proc. Natl. Acad. Sci. USA*, 89:

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6711 (1992); Sessa, W.C., et al., *J.Biol.Chem.*, 267: 15274
(1992); Geller, D.A., et al., *Proc. Natl. Acad. Sci. USA*,
90: 3491 (1993); Xie, Q. et al., *Science*, 256: 225-228
(1992)) neuronal, endothelial and macrophage, the former
5 two of which are constitutive and the latter of which is
inducible. The nomenclature for these different isoforms
used here is historical, as it is clear now that one or
more isoforms can be present in the same tissues (Dinerman,
J.L., et al., *Proc. Natl. Acad. Sci. USA*, 91: 4214-4218
10 (1994)).

As a diffusible free-radical gas, NO is a
multifunctional messenger affecting many aspects of
mammalian physiology [for reviews, see Dawson, T.M., et
al., *Ann. Neurol.* 32: 297 (1992); Nathan, C., *FASEB J.* 6:
15 3051 (1992); Moncada, S., et al., *N. Eng. J. Med.*, 329:
2002-2012 (1993); Michel, T., et al., *Amer. J. Cardiol.* 72:
33C (1993); Schuman, E.M., et al., *Annu. Rev. Neurosci.* 17:
153-183 (1994)]. NO originally was identified as an
endothelium-derived relaxing factor responsible for
20 regulation of vascular tone (Palmer, R.M.J., *Nature* 327:
524 (1987); Palmer, R.M.J., et al., *Nature* 333: 664 (1988);
Ignarro, L.J., et al., *Proc. Natl. Acad. Sci. USA*, 84: 9265
(1987)) and as a factor involved with macrophage-mediated
cytotoxicity (Marletta, M.A., et al., *Biochemistry* 21: 8706
25 (1988); Hibbs, J.B., et al., *Biochem. Biophys. Res. Comm.*
157: 87 (1989); Steuhr, D.J., et al., *J. Exp. Med.*, 169:
1543 (1989)). Since NO has been implicated in several
physiological processes including inhibition of platelet
aggregation, promotion of inflammation, inhibition of
30 lymphocyte proliferation and regulation of microcirculation
in kidney (Radomski, M., et al., *Proc. Natl. Acad. Sci. USA*
87: 5193 (1990); Albina, J.E., *J. Immunol.* 147: 144 (1991);
Katz, R., *Am. J. Physiol.* 261: F360 (1992); Ialenti, A., et
al., *Eur. J. Pharmacol.* 211: 177 (1992)). More recently,
35 NO also has been shown to play a role in cell-cell

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interactions in mammalian central and peripheral nervous systems -- in regulating neurotransmitter release, modulation of NMDA receptor-channel functions, neurotoxicity, nonadrenergic noncholinergic intestinal relaxation (Uemura, Y., et al., Ann. Neurol. 27: 620-625 (1990)) and activity-dependent regulation of neuronal gene expression (Uemura, Y., et al., Ann. Neurol. 27: 620 (1990); Dawson, V.L., et al., Proc. Natl. Acad. Sci. USA 88: 6368 (1991); Lei, S.Z., et al., Neuron 8: 1087 (1992); Prast, H., et al., Eur. J. Pharmacol. 216: 139 (1992); Peunova, N., Nature 364: 450 (1993)). Recent reports of NO function in synaptogenesis and in apoptosis during development of the rat CNS (Bredt, D.S., Neuron 13: 301 (1994); Roskams, A.J., Neuron 13: 289 (1994)) suggest that NO regulates activity-dependent mechanism(s) underlying the organization of fine-structure in the cortex (Edelman, G.M., et al., Proc. Natl. Acad. Sci. USA 89: 11651-11652 (1992)). NO also appears to be involved with long-term potentiation in hippocampus and long-term depression in cerebellum, two forms of synaptic plasticity that may underlie behavioral plasticity (Bohme, G.A., Eur. J. Pharmacol. 199: 379 (1991); Schuman, E.M., Science 254: 1503 (1991); O'Dell, T.J., et al., Proc. Natl. Acad. Sci. USA 88: 11285 (1991); Shibuki, K., Nature 349: 326 (1991); Haley, J.E., et al., Neuron 8: 211 (1992); Zhuo, M., Science 260: 1946 (1993); Zhuo, M., et al., NeuroReport 5: 1033 (1994)). Consistent with these cellular studies, inhibition of NOS activity has been shown to disrupt learning and memory (Chapman, P.F., et al., NeuroReport 3: 567 (1992); Holscher, C., Neurosci. Lett. 145: 165 (1992); Bohme, G.A., et al., Proc. Natl. Acad. Sci. USA 90: 9191 (1993); Rickard, N.S., Behav. Neurosci. 108: 640-644 (1994)).

Many of the above conclusions are based on pharmacological studies using inhibitors of nitric oxide

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synthases or donors of NO. Interpretations of such studies usually are limited because the drugs interact with more than one target and they cannot be delivered to specific sites. A molecular genetic approach can overcome these problems, however, by disrupting a specific gene, the product of which may be one of the drug's targets. Recently, such an approach has been attempted in mice via generation of a knock-out mutation of the neuronal NOS (nNOS) (Huang, P.L., et al., Cell 75: 1273-1286 (1993)).

5 While nNOS mutants appeared fully viable and fertile, minor defects in stomach morphology and hippocampal long-term potentiation were detected (Huang, P.L., et al., Cell 75: 1273-1286 (1993); O'Dell, T.J., et al., Science 265: 542-546 (1994)). Moreover, some NOS enzymatic activity still

15 was present in certain regions of the brain, suggesting a role for other NOS genes in the CNS. While yielding some relevant information about one specific component of NO function, this nNOS disruption existed throughout development. Consequently, functional defects of NOS

20 disruption in adults could not be resolved adequately from structural defects arising during development. Genetic tools exist in *Drosophila*, in contrast, to limit disruptions of gene functions temporally or spatially.

To identify candidate *Drosophila* NOS homologs, a

25 fragment of the rat neuronal NOS cDNA (Bredt, D.S., et al., Nature 351: 714-718 (1991)) was hybridized at low stringency to a phage library of the *Drosophila* genome as described in Example 11. The rat cDNA fragment encoded the binding domains of FAD and NADPH (amino acids 979 - 1408 of

30 SEQ ID NO.: 11), which are cofactors required for NOS activity, and therefore were expected to be conserved in fruit flies. Several *Drosophila* genomic clones were identified with the rat probe and classified into eight contigs. Sequence analysis of three restriction fragments

35 from these genomic clones revealed one (2.4R) with high

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homology to mammalian NOSs. The deduced amino acid sequence of the ORF encoded within the 2.4R fragment indicated 40% identity to the rat neuronal NOS and binding sites for FAD and NADPH.

5 The 2.4R DNA fragment then was used to probe a
 Drosophila adult head cDNA library as described in Example
 11, and eight clones were isolated. Restriction analysis
 indicated that all contained identical inserts and thus,
 defined a predominant transcript expressed by this
10 *Drosophila* gene. One clone (c5.3) was sequenced in both
 directions. The 4491 bp cDNA contained one long ORF of
 4350 bp. The methionine initiating this ORF was preceded
 by ACAAG which is a good match to the translation start
 consensus (A/CAAA/C) for *Drosophila* genes (Cavener, D.R.,
15 Nucleic Acids Res 15: 1353-1361 (1987)). Conceptual
 translation of this ORF yielded a protein of 1350 amino
 acids with a molecular weight of 151,842 Da.

 Comparison of the amino acid sequence of this deduced
 Drosophila protein (DNOS) (SEQ ID NO.: 9) to sequences of
20 mammalian NOSs revealed that DNOS is 43% identical to
 neuronal NOS (SEQ ID NO.: 11), 40% identical to endothelial
 NOS (SEQ ID NO.: 10) and 39% identical to macrophage NOS
 (SEQ ID NO.: 12). It also revealed similar structural
 motifs in DNOS (Figure 16A-16C). The C-terminal half of
25 the DNOS protein contains regions of high homology
 corresponding to the presumptive FMN-, FAD- and NADPH-
 binding sites. Amino acids thought to be important for
 making contacts with FAD and NADPH in mammalian NOSs
 (Bredt, D.S., et al., Nature 351: 714-718 (1991); Lamas,
30 S., et al., Proc. Natl. Acad. Sci. USA 89: 6348-6352 (1992);
 Lyons, C.R., et al., J. Biol. Chem. 267: 6370 (1992);
 Lowenstein, C.J., et al., Proc. Natl. Acad. Sci. USA 89:
 6711 (1992); Sessa, W.C., et al., J. Biol. Chem. 267: 15274
 (1992); Geller, D.A., et al., Proc. Natl. Acad. Sci. USA
35 90: 3491 (1993); Xie, Q. et al., Science 256: 225-228

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(1992)) are conserved in DNOS. The middle section of DNOS, between residues 215 and 746 of SEQ ID NO.: 9, showed the highest similarity to mammalian NOSs: it is 61% identical to the neuronal isoform and 53% identical to endothelial and macrophage isoforms. Sequences corresponding to the proposed heme- and calmodulin-binding sites in mammalian enzymes are well-conserved in DNOS. The region located between residues 643-671 of SEQ ID NO.: 9 has the characteristics of a calmodulin-binding domain (basic, amphiphilic α -helix) (O'Neil, K.T., et al., Trends Biochem. Sci. **15**: 59-64 (1990)). The amino acid sequence between these two sites is very well conserved among all four NOS proteins, suggesting the location of functionally important domains such as the arginine-binding site (Lamas, S., et al., Proc. Natl. Acad. Sci. USA **89**: 6348-6352 (1992)), tetrahydrobiopterine cofactor binding site or a dimerization domain. DNOS also has a PKA consensus site (Pearson, R.B., Meth. Enzymol. **200**: 62-81 (1991)) (at Ser-287 of SEQ ID NO.: 9) in a position similar to neuronal and endothelial NOSs.

The 214 amino acid N-terminal domain of DNOS shows no obvious homology to its equivalent portion of neuronal NOS or to the much shorter N-terminal domains of endothelial and macrophage NOSs. This region of DNOS contains an almost uninterrupted homopolymeric stretch of 24 glutamine residues. Such glutamine-rich domains, found in many *Drosophila* and vertebrate proteins, have been implicated in protein-protein interactions regulating the activation of transcription (Franks, R.G., Mech. Dev. **45**: 269 (1994); Gerber, H.-P., et al., Science **263**: 808 (1994); Regulski, M., et al., EMBO J. **6**: 767 (1987)). Thus, this domain of DNOS could be involved with protein-protein interactions necessary for localization and/or regulation of DNOS activity.

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The above sequence comparisons suggest that a *Drosophila* structural homolog of a vertebrate NOS gene was identified. The order of the putative functional domains in the DNOS protein is identical to that of mammalian enzymes (Figure 15B). Structural predictions based on several protein algorithms also indicate that general aspects of DNOS protein secondary structure (hydrophobicity plot, distribution of α -helices and β -strands) from the putative heme-binding domain to the C-terminus are similar to those of mammalian NOSs. DNOS also does not contain a transmembrane domain, as is the case for vertebrate NOSs. In addition to these general characteristics, several aspects of DNOS structure actually render it most like neuronal NOS: (i) the overall sequence similarity, (ii) the similarity of the putative calmodulin-binding site (55% identical to the neuronal NOS vs. 45% identical to endothelial NOS or vs. 27% identical to macrophage NOS) and (iii) the large N-terminal domain. Neuronal NOS and DNOS also do not contain sites for N-terminal myristoylation, which is the case for endothelial NOS (Lamas, S., et al., Proc. Natl. Acad. Sci. USA 89: 6348-6352 (1992)), nor do they have a deletion in the middle of the protein, which is the case for macrophage NOS (Xie, Q. et al., Science 256: 225-228 (1992)).

To establish that Applicants putative DNOS protein had nitric oxide synthase activity, the *dNOS* cDNA was expressed in 293 human embryonic kidney cells as described in Example 12, which have been used routinely in studies of mammalian NOSs (Bredt, D.S., et al., Nature 351: 714-718 (1991)). Protein extracts prepared from *dNOS*-transfected 293 cells as described in Example 12, contained a 150 kD polypeptide, which was recognized by a polyclonal antibody raised against the N-terminal domain of DNOS (Figure 17A, lane 293 + *dNOS*). This immunoreactive polypeptide was of a size expected for DNOS and was absent from cells transfected

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with just the pCGN vector alone (Figure 17A, lane 293 + vector).

Extracts made from dNOS-transfected 293 cells showed significant NO synthase activity, as measured by the L-arginine to L-citrulline conversion assay as described in Example 12 (0.1276 ± 0.002 pmol/mg/min; Figure 17B, group B). [In a parallel experiment, the specific activity of rat neuronal NOS expressed from the same vector in 293 cells was 3.0 ± 0.02 pmol/mg/min, N=4]. DNOS activity was dependent on exogenous Ca^{2+} /calmodulin and on NADPH, two cofactors necessary for activity of constitutive mammalian NOSs (Iyengar, R., Proc. Natl. Acad. Sci. USA **84**: 6369-6373 (1987); Bredt, D.S., Proc. Natl. Acad. Sci. USA **87**: 682-685 (1990)). DNOS activity was reduced 90% by the Ca^{2+} chelator EGTA (Figure 17B, group C). Also, $500\mu\text{M}$ N-(6-aminohexyl)-1-naphthalene-sulfonamide (W5), a calmodulin antagonist which inhibits activity of neuronal NOS (Bredt, D.S., Proc. Natl. Acad. Sci. USA **87**: 682-685 (1990)), diminished DNOS activity to 18% (0.0222 ± 0.001 pmol/mg/min, N=2). In the absence of exogenous NADPH, DNOS (or nNOS) activity was reduced 20% (0.1061 ± 0.011 pmol/mg/min, N=4 for DNOS; 2.7935 ± 0.033 pmol/mg/min, N=2 for nNOS). DNOS activity also was blocked by inhibitors of mammalian NOSs (Rees, D.D., Br. J. Pharmacol., **101**: 746-752 (1990)). N^G -nitro-L-arginine methyl ester (L-NAME) reduced DNOS activity 84% (Figure 17B, group D), and $100\mu\text{M}$ N^G -monomethyl-L-arginine acetate produced a complete block (0.0001 ± 0.0002 pmol/mg/min, N=2). These enzymatic data demonstrate that DNOS is a Ca^{2+} /calmodulin-dependent nitric oxide synthase.

Northern blot analysis indicated a 5.0 kb dNOS transcript which was expressed predominantly in adult fly heads but not bodies (Figure 18A). More sensitive RT-PCR experiments as described in Example 13, however, detected dNOS message in poly(A)⁺ RNA from fly bodies. Neuronal NOS

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genes from mice and humans produce two alternatively spliced transcripts, the shorter one of which yields a protein containing a 105 amino acid in-frame deletion (residues 504-608 in mouse or rat neuronal NOS) (Ogura, T.,
5 Biochem. Biophys. Res. Commun. 193: 1014-1022 (1993)). RT-PCR amplification of *Drosophila* head mRNA produced two DNA fragments: the 444 bp fragment corresponded to vertebrate long form and the 129 bp fragment corresponded to vertebrate short form (Figure 18B). Conceptual translation
10 of the 129 bp sequence confirmed a splicing pattern identical to that for the nNOS gene (Figure 18C). Presence of the short NOS isoform in *Drosophila* strengthens the notion that it may play an important role in NOS biochemistry.

15 The discovery of a NOS homolog in *Drosophila* provides definitive proof that invertebrates produce NO and, as suggested by recent reports, most likely use it for intercellular signaling. These data also suggest that a NOS gene was present in an ancestor common to vertebrates
20 and arthropods, implying that NOS has existed for at least 600 million years. Thus, it is expected that NOS genes are prevalent throughout the animal kingdom.

Consistent with this view are existing histochemical data. NOS activity has been detected in several
25 invertebrate tissue extracts: in *Lymulus polyphemus* Radomski, M.W., Philos. Trans. R. Soc. Lond. B. Biol. Sci., 334: 129-133 (1992)), in the locust brain (Elphick, M.R., et al., Brain Res. 619: 344-346 (1993)), in the salivary gland of *Rhodnius prolixus* (Ribeiro, J.M.C., et al., FEBS
30 Let. 330: 165-168 (1993) (34)) and in various tissues of *Lymnaea stagnalis* (Elofsson, R., et al., NeuroReport 4: 279-282 (1993)). Applications of NOS inhibitors or NO-generating substances have been shown to modulate the activity of buccal motoneurons in *Lymnaea stagnalis*
35 (Elofsson, R., et al., NeuroReport 4: 279-282 (1993)) and

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the oscillatory dynamics of olfactory neurons in procerebral lobe of *Limax maximus* (Gelperin, A., Nature 369: 61-63 (1994)). NADPH-diaphorase staining, a relatively specific indicator of NOS protein in fixed
5 vertebrate tissue samples (Dawson, T.M., et al., Proc. Natl. Acad. Sci. USA 88: 7797 (1991); Hope, B.T., et al., Proc. Natl. Acad. Sci. USA 88: 2811 (1991)), also has suggested the presence of NOS in *Drosophila* heads (Muller, U., Naturwissenschaft 80: 524-526 (1993)). The present
10 molecular cloning of *dNOS* considerably strengthens the validity of these observations.

Sophisticated genetic analyses of NOS function are available in *Drosophila*. Classical genetics will allow the creation of point mutations and deletions in *dNOS*,
15 resulting in full or partial loss of *dNOS* function. Such mutations will permit detailed studies of the role of NOS during development.

The invention further relates to isolated DNA that are characterized by their ability to encode a polypeptide
20 of the amino acid sequence in Figure 16A-16C (SEQ ID NO.: 9) or functional equivalents thereof (i.e., a polypeptide which synthesizes nitric oxide). Isolated DNA meeting this criteria comprise amino acids having sequences homologous to sequences of mammalian NOS gene products (i.e.,
25 neuronal, endothelial and macrophage NOSs). The DNA sequence represented in SEQ ID NO.: 25 is an example of such an isolated DNA. Isolated DNA meeting these criteria also comprise amino acids having sequences identical to sequences of naturally occurring *dNOS* or portions thereof,
30 or variants of the naturally occurring sequences. Such variants include mutants differing by the addition, deletion or substitution of one or more residues, modified nucleic acids in which one or more residues is modified (e.g., DNA or RNA analogs), and mutants comprising one or
35 more modified residues.

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Such nucleic acids can be detected and isolated under high stringency conditions or moderate stringency conditions, for example. "High stringency conditions" and "moderate stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 (see particularly 2.10.8-11) and pages 6.3.1-6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. et al., eds, Vol. 1, Suppl. 26, 1991), the teachings of which are incorporated herein by reference. Factors such as probe length, base composition, percent mismatch between the hybridizing sequences, temperature and ionic strength influence the stability of nucleic acid hybrids. Thus, high or moderate stringency conditions can be determined empirically, depending in part upon the characteristics of the known DNA to which other unknown nucleic acids are being compared for homology.

Isolated DNA that are characterized by their ability to encode a polypeptide of the amino acid sequence in Figure 16A-16C, encode a protein or polypeptide having at least one function of a *Drosophila* NOS, such as a catalytic activity (e.g., synthesis of nitric oxide) and/or binding function (e.g., putative heme, calmodulin, FMN, FAD and NADPH binding). The catalytic or binding function of a protein or polypeptide encoded by hybridizing nucleic acid may be detected by standard enzymatic assays for activity or binding (e.g., assays which monitor conversion of L-arginine to L-citrulline). Functions characteristic of dNOS may also be assessed by in vivo complementation activity or other suitable methods. Enzymatic assays, complementation tests, or other suitable methods can also be used in procedures for the identification and/or isolation of nucleic acids which encode a polypeptide having the amino acid sequence in Figure 16A-16C or functional equivalents thereof.

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The present invention will now be illustrated by the following examples, which are not intended to be limiting in any way.

EXAMPLES

- 5 The following materials and methods were used in the work described in Examples 1 and 2.

Expression Cloning of dCREB1 and dCREB2

- Standard protocols for expression cloning by DNA-binding (Ausubel, F., Current Protocols in Molecular
10 Biology, John Wiley and Sons, New York, 1994; Singh, H. et al., Cell, 52: 415-423 (1988)) were followed except as noted. A double-stranded, 3xCRE oligonucleotide was synthesized and cloned between the XbaI and KpnI sites of pGEM7Zf+ (Promega). The sequence of one strand of the
15 oligonucleotide was 5' CGTCTAGATCTATGACTGAATA TGACGTAATATGACGTAATGGTACCAGATCTGGCC 3' (SEQ ID NO.: 17), with the CRE sites underlined. The oligonucleotide was excised as a BglII/HindIII fragment and labeled by filling-in the overhanging ends with Klenow fragment in the
20 presence of [α^{32} P]dGTP, [α^{32} P]dCTP and unlabeled dATP and dTTP (Ausubel, F., Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1994)). Just prior to use, the labeled fragment was pre-absorbed to blank nitrocellulose filters to reduce background binding. All
25 other steps were as described (Ausubel, F., Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1994)). After secondary and tertiary lifts, positive clones were subcloned into pKS+ (Stratagene) and sequenced.

Gel Shift Analysis

- 30 Gel-mobility shift assays were performed as in Ausubel, F., Current Protocols in Molecular Biology, John

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Wiley and Sons, New York, 1994, with the following modifications. The 4% polyacrylamide gel (crosslinking ratio 80:1) was cast and run using 5x Tris-glycine buffer (Ausubel, F., Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1994)) supplemented with 3mM MgCl₂. The oligonucleotides used as the DNA probes were boiled and slowly cooled to room temperature at a concentration of 50 µg/ml in 0.1M NaCl. 50 ng of double-stranded probe was end-labeled using polynucleotide kinase in the presence of 100 µCi of [γ^{32} P]ATP. The double-stranded oligonucleotides were purified on a native polyacrylamide gel and used in a mobility shift assay at about 0.5 ng/reaction.

For dCREB2, the original dCREB2-b cDNA was subcloned and subjected to site-directed mutagenesis to introduce restriction sites immediately 5' and 3' of the open reading frame. This open reading frame was subcloned into the pET11A expression vector (Novagen) and used to induce expression of the protein in bacteria. The cells containing this vector were grown at 30°C to an approximate density of 2×10^8 /ml and heat-induced at 37°C for 2 hours. The cells were collected by centrifugation and lysed according to Buratowski, S. et al., Proc. Natl. Acad. Sci. USA, **88**: 7509-7513 (1991). The crude extract was clarified by centrifugation and loaded onto a DEAE column previously equilibrated with 50 mM TrisHCl, pH 8.0, 10% sucrose, 100 mM KCl. Step elutions with increasing amounts of KCl in the same buffer were used to elute the dCREB2-b protein, which was assayed using the gel mobility-shift assay. The peak fraction was dialyzed against the loading buffer and used in the binding experiment. The specific competitor that was used was the wild-type CRE oligonucleotide. The sequence of one strand of the double-stranded oligonucleotides used in the gel shift analysis are listed.

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For the first two oligonucleotides, wild-type and mutant CREs are underlined.

Wild-type 3xCRE (SEQ ID NO.: 18):

5' AAATGACGTAACGGAAATGACGTAACGGAAATGACGTAACG 3';

5 Mutant 3xmCRE (SEQ ID NO.: 19):

5' AAATGAATTAAACGGAAATGAATTAAACGGAAATGAATTAAACGG 3';

Nonspecific competitor #1 (SEQ ID NO.: 20):

5' TGCACGGGTTTTTCGACGTTCACTGGTAGTGTCTGATGAGGCCGAAAGGCCGAAA
CGCGATGCCCATACCACCGCTCAG 3';

10 Nonspecific competitor #2 (SEQ ID NO.: 21):

5' TCGACCCACAGTTTTCGGGTTTTTCGAGCAAGTCTGCTAGTGTCTGATGAGGCCG
AAAGGCCGAAACGCGAAGCCGTATTGCACCACGCTCATCGAGAAGGC 3';

Nonspecific competitor #3 (SEQ ID NO.: 22):

5' CTAGAGCTTGCAAGCATGCTTGCAAGCAAGCATGCTTGCAAGCATGCTTG
15 CAAGC 3';

Nonspecific competitor #4 (SEQ ID NO.: 23):

5' CTCTAGAGCGTACGCAAGCGTACGCAAGCGTACG 3'

For dCREB1, heat-induced bacterial extracts (Ausubel, F., Current Protocols in Molecular Biology, John Wiley and
20 Sons, New York, 1994) were made from the original phage
clone integrated by lysogeny. Extract from a bacteria
lysogenized with another plaque (which did not bind to CRE
sites) from the screen was used as a negative control.
Competition experiments were done using a 4-100 fold molar
25 excess (relative to the probe) of unlabeled, wild-type CRE
oligonucleotides or unlabeled, mutant CRE oligonucleotides.

Northern Blots

Total head and body RNA was isolated from flies
according to the protocol of Drain, P. et al., Neuron,
30 6:71-82 (1991).. Total RNA from all other developmental
stages was a gift from Eric Schaeffer. All RNA samples
were selected twice on oligo-dT columns (5 Prime-3 Prime)
to isolate poly A+ RNA. Two µg of poly A+ RNA was
fractionated on 1.2% formaldehyde-formamide agarose gels,

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transferred to nitrocellulose and probed using an uniformly labeled, strand-specific, antisense RNA (aRNA) probe. The template for the synthesis of aRNA was one of the partial cDNA clones isolated from the library screen (pJY199).

- 5 This cDNA contained the carboxyl-terminal 86 amino acids of the dCREB2-b protein and about 585 bp of 3' untranslated mRNA. All Northern blots were washed at high stringency (0.1% SDS, 0.1xSSC, 65°C).

In situ Hybridization To Tissue Sections

- 10 Frozen frontal sections were cut and processed under RNase-free conditions, essentially as described in Nighorn, A. et al., Neuron, 6:455-467 (1991), with modifications for riboprobes as noted here. Digoxigenin-labeled riboprobes were made from pJY199 using the Genius kit (Boehringer-Mannheim).
- 15 One μ g of Xba-linearized template and T3 RNA polymerase was used to make the antisense probe, while one μ g of EcoRI-linearized template together with T7 RNA polymerase was used for the control sense probe. Alkaline hydrolysis (30 minutes at 60°C) was used to reduce the average probe size to about 200 bases. The hydrolyzed probe was diluted 1:250 in hybridization solution (Nighorn, A. et al., Neuron, 6:455-467 (1991)), boiled, quickly cooled on ice, added to the slides and hybridized at 42°C overnight. The slides were then treated with RNase A (20 μ g/ml RNase A in 0.5 M NaCl/10 mM Tris pH8 for 1 hour at 37°C) prior to two 50°C washes. Digoxigenin detection was as described.
- 25

Reverse Transcription Coupled With the Polymerase Chain Reaction (RT-PCR) Analysis of dCREB2 and Identification of

30 Alternatively Spliced Exons

The template for reverse transcription coupled with the polymerase chain reaction (RT-PCR) was total RNA or poly A+ RNA isolated from *Drosophila* heads as in Drain, P.

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et al., Neuron, 6: 71-82 (1991). Total RNA used was exhaustively digested with RNase-free DNase I (50 µg of RNA digested with 50 units of DNase I for 60-90' at 37°C followed by phenol, phenol/chloroform extraction, and ethanol precipitation) prior to use. Results from separate experiments indicate that this DNase-treatment effectively eliminates the possibility of PCR products derived from any contaminating genomic DNA. Two rounds of selection using commercial oligo-dT columns (5 Prime-3 Prime) were used to isolate poly A+ RNA from total RNA. The template for an individual reaction was either 100-200 ng of total RNA, or 10-20 ng of poly A+ RNA.

The RT-PCR reactions were performed following the specifications of the supplier (Perkin-Elmer) with a "Hot Start" modification (Perkin-Elmer RT-PCR kit instructions). All components of the RT reaction, except the rTth enzyme, were assembled at 75°C, and the reaction was initiated by adding the enzyme and lowering the temperature to 70°C. At the end of 15 minutes, the preheated (to 75°C) PCR components (including trace amounts of [α^{32} P]dCTP) were added quickly, the reaction tubes were put into a pre-heated thermocycler, and the PCR amplification begun. Cycling parameters for reactions (100 µl total volume) in a Perkin-Elmer 480 thermocycler were 94°C for 60 seconds, followed by 70°C for 90 seconds. For reactions (50µl) in an MJ Minicycler the parameters were 94°C for 45 seconds and 70°C for 90 seconds.

All primers used in these procedures were designed to have 26 nucleotides complementary to their target sequence. Some primers had additional nucleotides for restriction sites at their 5' ends to facilitate subsequent cloning of the products. Primers were designed to have about 50% GC content, with a G or C nucleotide at their 3' most end and with no G/C runs longer than 3. For RT-PCR reactions with a given pair of primers, the Mg²⁺ concentration was

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optimized by running a series of pilot reactions, at Mg^{+2} concentrations ranging from 0.6 mM to 3.0 mM. Reaction products were analyzed on denaturing urea-polyacrylamide gels by autoradiography. Any product that appeared larger
5 than the band predicted from the cDNA sequence was purified from a preparative native gel, re-amplified using the same primers, gel-purified, subcloned and sequenced.

To verify that a given RT-PCR product was truly derived from RNA, control reactions were run to show that
10 the appearance of the product was eliminated by RNase A treatment of the template RNA. Also, products generated from reactions using total RNA as the template were re-isolated from reactions using twice-selected polyA+RNA as template.

15 Plasmids

Expression constructs for transient transfection experiments in *Drosophila* were made in the expression vector pAct5CPPA (Han, K. et al., *Cell*, 56: 573-583 (1989)) or in pAcQ. pAcQ is a close derivative of pAct5CPPA in
20 which the XbaI site at the 5' end of the 2.5 kb actin promoter fragment was destroyed and additional sites were inserted in the polylinker. pAc-dCREB1 was made by subcloning a KpnI-SacI fragment containing the complete dCREB1 open reading frame (from a cDNA subcloned into pKS+) into pAct5CPPA. pAc-PKA was constructed by subcloning an
25 EcoRV fragment encoding the *Drosophila* PKA catalytic subunit (Foster, J.L. et al., *J. Biol. Chem.*, 263: 1676-1681 (1988)) from a modified pHSREM1 construct (Drain, P. et al., *Neuron*, 6: 71-82 (1991)) into pAct5CPPA. To make
30 the 3xCRE-lacZ reporter construct for *Drosophila* cell culture, the double-stranded, wild-type 3xCRE oligonucleotide used in the gel shift analysis was cloned into the KpnI-XbaI backbone of HZ50PL (Hiromi, Y. and W.J. Gehring, *Cell*, 50: 963-974 (1987)), a reporter construct

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made for enhancer testing which has cloning sites in front of a minimal *hsp70* promoter-lacZ fusion gene.

RSV-dCREB2-a was constructed in a long series of cloning steps. Essentially, the activator-encoding open reading frame was first reconstructed on the plasmid pKS+ by sequentially adding each of the three exons (exons 2, 4 and 6) into the original cDNA of dCREB2-b, which had been subcloned from phage DNA into pKS+. Site-directed mutagenesis was used to introduce unique restriction enzyme sites both 5' and 3' of the dCREB2-b open reading frame, and these sites facilitated the subcloning process and allowed removal of 5' and 3' untranslated sequences. Once the activator was assembled, the resulting open reading frame was sequenced to confirm the cloning steps and moved into a modified RSV vector which contained a polylinker located between the RSV promoter and the SV40 polyadenylation sequences (RSV-0). RSV-dCREB2-b was made by moving the original dCREB2-b cDNA (which had been subcloned into pKS+) into RSV-0.

Other constructs used in experiments were: pCaE (pMtC) (Mellon, P.L. et al., *Proc. Natl. Acad. Sci. USA*, 86: 4887-4891 (1989)), which contains the cDNA for mouse PKA catalytic subunit cloned under the mouse metallothionein 1 promoter; RSV- β gal (Edlund, T. et al., *Science*, 230: 912-916 (1985)), which expresses the lacZ gene under control of the Rous sarcoma long terminal repeat promoter (Gorman, C.M. et al., *Proc. Natl. Acad. Sci. USA*, 79: 6777-6781 (1982)). RSV-CREB (Gonzalez, G.A. et al., *Nature*, 337: 749-752 (1989)) is a CREB cDNA fragment containing the 341-amino acid open reading frame under the RSV LTR-promoter in RSV-SG, and the D(-71) CAT reporter (Montminy, M.R. et al., *Proc. Natl. Acad. Sci. USA*, 83: 6682-6686 (1986)) which is a fusion of a CRE-containing fragment of the rat somatostatin promoter and the bacterial CAT coding region.

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F9 Cell Culture and Transfection

Undifferentiated F9 cells were maintained and transfected using the calcium phosphate method as described in Darrow, A.L. et al., "Maintenance and Use of F9 Teratocarcinoma Cells" In *Meth. Enzymol.*, v. 190 (1990), except that chloroquine was added to 100 mM immediately before transfection and precipitates were washed off ten hours after transfection, at which time the dishes received fresh chloroquine-free medium. Amounts of DNA in transfections were made equivalent by adding RSV-0 where required. Cells were harvested 30 hours after transfection. Extracts were made by three cycles of freeze/thawing, with brief vortexing between cycles. Particulate matter was cleared from extracts by ten minutes of centrifugation in the cold. β -galactosidase assays were performed as described in Miller, J.H., *Experiments in Molecular Genetics*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1972. CAT assays were performed as described in Sheen, J.Y. and B. Seed, *Gene*, 67: 271-277 (1988) using aliquots of extract heat-treated at 65°C for ten minutes and centrifuged for ten minutes to remove debris. Results reported are from three experiments run on different days with at least three dishes per condition within each experiment. Error bars represent standard error of the mean, with error propagation taken into account (Grossman, M. and H.W. Norton, *J. Hered.*, 71: 295-297 (1980)).

Drosophila Cell Culture and Transient Transfection

Schneider L2 cells in Schneider's medium (Sigma) supplemented with 10% fetal bovine serum (FBS) or Kc167 cells in D-22 medium (Sigma) supplemented with 10% FBS, were transfected by the calcium phosphate method essentially as described in Krasnow, M.A. et al., *Cell*, 57: 1031-1043 (1989), with the following differences. Kc167 cells were plated at 2×10^6 cells/ml and chloroquine was

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added to a final concentration of 100 mM immediately prior to transfection. A total of 10 µg of plasmid DNA per dish was used for L2 transfections and 25 µg per dish for Kc167 transfections. DNA masses in transfections were made equivalent with pGEM7Zf+ where required. Precipitates were left undisturbed on L2 cells until harvest, but for Kc167 cells the original medium was replaced with fresh, chloroquine-free medium after twelve hours. Cells were harvested thirty-six to forty-eight hours after transfection. Extracts were made and enzymatic assays performed as described above for F9 cells. Results reported for transfections are averages of at least three experiments run on different days, with at least duplicate dishes for each condition within experiments. Error bars represent standard error of the mean, with error propagation taken into account (Grossman, M. and H.W. Norton, *J. Hered.*, 71: 295-297 (1980)).

β-galactosidase (βgal) and Chloramphenicol Acetyl Transferase (CAT) Assays

β-galactosidase assays were run and activity calculated as described in Miller, J.H., *Experiments in Molecular Genetics*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1972. CAT assays were performed essentially according to Sheen, J.Y. and B. Seed, *Gene*, 67: 271-277 (1988)) using supernatants from heat-treated aliquots of extracts (65°C for 10 minutes and then centrifuged for 10 minutes). Relative activity was calculated according to Sheen, J.Y. and B. Seed, *Gene*, 67: 271-277 (1988)).

PKA-Responsive Transcriptional Activation by dCREB2-a

F9 cells were transiently transfected with 10 µg of D(-71) CAT plasmid as a CRE-directed reporter. 5 µg of RSV-βgal reporter was included in each dish as a

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normalization control for transfection efficiency.

Different groups received 8 μ g of dCREB2-a expression vector and 4 μ g of PKA expression vector, separately or in combination. Results are expressed as CAT/ β gal enzyme activity ratios, standardized to values obtained with PKA-transfected dishes.

Transcriptional Effect of dCREB2-b and a Mutant Variant On PKA-Responsive Activation by dCREB2-a

F9 cells were transiently cotransfected with 10 μ g of D(-71) CAT along with the indicated combinations of the following expression constructs: RSV-dCREB2-a (5 μ g); pMtC (2 μ g); RSV-dCREB2-b (5 μ g); and RSV-mLZ-dCREB2-b, which expresses a leucine-zipper mutant of dCREB2-b (5 μ g). The DNA mass for each dish was made up to 27 μ g with RSV-O.

Other experimental conditions are as described above under "PKA-Responsive Transcriptional Activation by dCREB2-a".

Transcriptional Activation of a CRE Reporter Gene by dCREB1 in Drosophila Schneider L2 cell culture

The cells were transiently transfected with a dCREB1 expression construct (1 μ g), with or without a construct which expresses Drosophila PKA. 3xCRE- β gal reporter (1 μ g) and the normalization Ac-CAT reporter (1 μ g) were included in each dish. Expression vectors not present in particular dishes were replaced by pACQ.

Example 1 Isolation and Characterization of dCREB2

Two different genes were isolated in a DNA-binding expression screen of a Drosophila head cDNA library using a probe containing three CRE sites (3xCRE). Many clones were obtained for the dCREB2 gene, while only one clone was obtained for dCREB1. The dCREB2 clones had two alternatively-spliced open reading frames, dCREB2-b and dCREB2-c (see Figure 2). These differed only in the

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presence or absence of exon 4 and in their 5' and 3' untranslated regions. The inferred translation product of dCREB2-b showed very high sequence similarity to the amino acid sequences of the basic region/leucine zipper (bZIP) domains of mammalian CREB (SEQ ID NO.: 4), CREM (SEQ ID NO.: 5) and ATF-1 (SEQ ID NO.: 6) (see Figure 1B).

Chromosomal *in situ* hybridization using a dCREB2 probe localized the gene to a diffuse band at 17A2 on the X chromosome, a region which contains several lethal complementation groups (Eberl, D.F. et al., *Genetics*, 30: 569-583 (1992)).

To determine the DNA binding properties of dCREB2-b, the DNA binding activity of dCREB2-b was assayed using a gel mobility-shift assay. Bacterial extracts expressing the dCREB2-b protein retarded the migration of a triplicated CRE probe (3xCRE). The protein had lower, but detectable, affinity for a mutated 3xCRE oligonucleotide. Competition experiments using unlabeled competitor oligonucleotides showed that the binding of dCREB2-b to 3xCRE was specific with higher affinity for CRE sites than to nonspecific DNA. Together with the conserved amino acid sequence, this functional similarity suggested that dCREB2 was a CREB family member.

The expression pattern of dCREB2 was determined by Northern blot analysis of poly A+RNA from various developmental stages. A complex pattern with at least 12 different transcript sizes was found. Two bands of approximately 0.8 and 3.5 kb were common to all of the stages. The adult head contained transcripts of at least six sizes (0.8, 1.2, 1.6, 1.9, 2.3 and 3.5 kb). *In situ* hybridization to RNA in *Drosophila* head tissue sections showed staining in all cells. In the brain, cell bodies but not neuropil were stained.

dCREB2 has alternatively-spliced forms. Initial transfection experiments showed that the dCREB2-c isoform

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was not a PKA-responsive transcriptional activator. This information, together with the complex developmental expression pattern and the known use of alternative splicing of the CREM gene to generate PKA-responsive
5 activators (Foulkes, N. and P. Sassone-Corsi, *Cell*, 68: 411-414 (1992); Foulkes, N.S. et al., *Nature*, 355: 80-84 (1992)) suggested that additional domains might be required to code for an activator.

Reverse transcription coupled with the polymerase
10 chain reaction (RT-PCR) was used to identify new exons. Comparison of the genomic DNA sequence with that of cDNAs indicated the general exon/intron organization and assisted in the search for additional exons. Sense and antisense primers spaced across the dCREB2-b cDNA were synthesized
15 and used pairwise in RT-PCR reactions primed with *Drosophila* head RNA. Reactions with primers in exons 5 and 7 (see Figure 2) generated two products, one with the predicted size (compared with the cDNA clones) and one that was larger. The larger fragment was cloned and its
20 sequence suggested the presence of exon 6 (see Figure 1A; SEQ ID NO.: 1). A primer within exon 6 was synthesized, end-labeled and used to screen a *Drosophila* head cDNA library. Two clones were isolated, sequenced and found to be identical. This splicing isoform, dCREB2-d, confirmed
25 the splice junctions and exon sequence inferred from the RT-PCR products.

Initial attempts to isolate exon 2 proved difficult. The genomic sequence that separated exons 1 and 3 (see Figure 2) was examined and one relatively extensive open
30 reading frame (ORF) was identified. Three antisense primers, only one of which lay inside this ORF, were synthesized based on the intron sequence. Three sets of RT-PCR reactions were run in parallel, each using one of the three antisense primers and a sense primer in exon 1.
35 Only the reaction that used the antisense primer in the ORF

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produced a PCR product. The sequence of this product matched a continuous stretch of nucleotides from the genomic sequence, extending 3' from exon 1 past the splice junction in the *dCREB2-b* cDNA to the location of the antisense primer in the ORF. This fragment suggested that exon 1 might be extended in some mRNAs by use of an alternative 5' splice site located 3' to the site used to make *dCREB2-b*. Based on the newly-identified exon sequences, a sense primer was made. This primer was used with an antisense primer in exon 3 to generate a new product whose sequence established the location of the new 5' splice site. The sequence added to exon 1 by alternative 5' splice site selection is denoted exon 2. The exon 2 sequence also showed that the same 3' splice site was used both for the original cDNA and for exon 2. To independently verify this alternative splicing pattern, RT-PCR was carried out with a primer that spanned the 3' splice junction of exon 2 and a primer in exon 1. The sequence of the product corroborated the splice junctions of exon 2 shown in Figure 1A (SEQ ID NO.: 1).

To determine if exons 2 and 6 could be spliced into the same molecule, an RT-PCR reaction was carried out with primers in exons 2 and 6. The reaction produced a product of the size predicted by coordinate splicing of these two exons and the identity of this product was confirmed by extensive restriction analysis.

dCREB2 is a *Drosophila* CREB/ATF gene. Figure 1A shows the DNA sequence (SEQ ID NO.: 1) and inferred amino acid sequence (SEQ ID NO.: 2) of *dCREB2-a*, the longest ORF that can result from the identified alternative splicing events. The indicated translation start site for this ORF is probably authentic because: i) stop codons occur upstream from this ATG in all reading frames in our *dCREB2* cDNAs (sequences not shown) ii) this ATG was selected by computer (Sheen, J.Y. and B. Seed, *Gene*, 67: 271-277 (1988)) as the

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best ribosome binding site in the DNA sequence that contains the ORF; and iii) use of the next ATG in the open reading frame 480 nucleotides downstream would not produce an inferred product that is a PKA-dependent activator (see
5 below). This information does not exclude the possibility that internal translation initiation sites may be used in this transcript, as happens in the CREM gene's S-CREM isoform (Delmas, V. et al., *Proc. Natl. Acad. Sci. USA*, 89: 4226-4230 (1992)).

10 The dCREB2-a open reading frame predicts a protein of 361 amino acids with a carboxyl-terminal bZIP domain (SEQ ID NO.: 3) highly homologous to those of mammalian CREB (SEQ ID NO.: 4) and CREM (SEQ ID NO.: 5) (see Figure 1B). The inferred dCREB2-a product has a small region of amino
15 acids containing consensus phosphorylation sites for PKA, calcium/calmodulin-dependent kinase II (CaM kinase II) and protein kinase C (PKC) at a position similar to that of the P-box in CREB, CREM and ATF-1. The amino-terminal third of the predicted dCREB2-a is rich in glutamines (including
20 runs of four and five residues). Glutamine-rich activation domains occur in CREB, CREM, and other eukaryotic transcription factors, including some from *Drosophila* (Courey, A.J. and R. Tijan, "Mechanisms of Transcriptional Control as Revealed by Studies of the Human Transcription
25 Factor Sp1" *In Transcriptional Regulation*, vol. 2, McKnight, S.L. and K.R. Yamamoto (eds.), Cold Spring Harbor Press, Cold Spring Harbor, NY, 1992; Mitchell, P.J. and R. Tijan, *Science*, 245: 371-378 (1989)).

A computerized amino acid sequence homology search
30 with the predicted dCREB2-a protein sequence (SEQ ID NO.: 2) identifies CREB, CREM and ATF-1 gene products as the closest matches to dCREB2-a. The homology is particularly striking in the carboxyl-terminal bZIP domain where 49 of 54 amino acids are identical with their
35 counterparts in mammalian CREB (Figure 1B). The homology

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is less striking, albeit substantial, in the activation domain. Lower conservation in this domain is also characteristic of the mammalian CREB and CREM genes (Masquillier, D. et al., *Cell Growth Differ.*, 4: 931-937 (1993)).

Figure 2 shows the exon organization of all of the dCREB2 alternative splice forms that we have detected, both as cDNAs and by RT-PCR. Splice products of dCREB2 fall into two broad categories. One class of transcripts (dCREB2-a, -b, -c, -d) employs alternative splicing of exons 2, 4 and 6 to produce isoforms whose protein products all have the bZIP domains attached to different versions of the activation domain. The second class of transcripts (dCREB2-q, -r, -s) all have splice sites which result in in-frame stop codons at various positions upstream of the bZIP domain. These all predict truncated activation domains without dimerization or DNA binding activity.

Two different dCREB2 isoforms, dCREB2-a and dCREB2-b, have opposite roles in PKA-responsive transcription. The capacity of isoforms of the dCREB2 gene to mediate PKA-responsive transcription was tested in F9 cells. These cells have been used extensively to study CREB-dependent activation because their endogenous cAMP-responsive transcription system is inactive (Gonzalez, G.A. et al., *Nature*, 337: 749-752 (1989); Masson, N. et al., *Mol. Cell Biol.*, 12: 1096-1106 (1992); Masson, N. et al., *Nucleic Acids Res.*, 21: 1163-1169 (1993)). Candidate cAMP-responsive transcription factors, synthesized from expression vectors, were transiently transfected with and without a construct expressing the PKA catalytic subunit. CREB-dependent changes in gene expression were measured using a cotransfected construct that has a CRE-containing promoter fused to a reporter gene.

The product of the dCREB2-a isoform is a PKA-dependent activator of transcription (Figure 3). Transfection of PKA

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or dCREB2-a alone gave only modest activation above baseline values. Cotransfection of dCREB2-a and PKA together, however, gave levels of activation 5.4-fold greater than the activation seen with PKA alone.

5 dCREB2-b did not act as a PKA-dependent transactivator. When transfected together with the reporter and PKA, it failed to stimulate reporter activity. Instead, it functioned as a direct antagonist of PKA-dependent activation by dCREB2-a (Figure 4). Cotransfection
10 of equimolar amounts of the dCREB2-a and dCREB2-b expression constructs, along with PKA and the reporter, resulted in a nearly complete block of PKA-dependent activation from the CRE-containing reporter.

The strong homology between the leucine zippers of
15 dCREB2 (SEQ ID NO.: 3), CREB (SEQ ID NO.: 4) and CREM (SEQ ID NO.: 5) (see Figure 1B) suggested that mutations which abolish CREB dimerization (Dwarki, V.J. et al., EMBO J., 9: 225-232 (1990)) should also affect dCREB2 dimerization. The mutant *Drosophila* molecule mLZ-dCREB2-b was made by
20 introducing two single-base changes that convert the middle two leucines of the leucine zipper to valines. An identical mutation in CREB abolishes homodimerization in vitro (Dwarki, V.J. et al., EMBO J., 9: 225-232 (1990)). Cotransfected mLZ-dCREB2-b failed to block PKA-dependent
25 activation by dCREB2-a (Figure 4).

Example 2 Isolation and Characterization of dCREB1

A single cDNA representing the dCREB1 gene was isolated in the same screen of a *Drosophila* lambda gt11 expression library that yielded the dCREB2 cDNAs. The
30 sequence of the dCREB1 cDNA contained a complete open reading frame specifying a 266 amino acid protein with a carboxyl-terminal leucine zipper four repeats long and an adjacent basic region (Figure 5; SEQ ID NO.: 7). The amino-terminal half of the inferred protein contains an

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acid-rich activation domain, with glutamate, aspartate and proline residues spaced throughout. dCREB1 has consensus phosphorylation sites for CaM kinase II and PKC throughout its length, but has no predicted phosphoacceptor site for
5 PKA.

Gel shift analysis showed higher-affinity binding of the dCREB1 protein to 3xCRE than to 3xmCRE. Transcriptional activation by dCREB1 was assayed with transient cotransfection experiments using the *Drosophila*
10 L2 and Kc167 cell culture lines. In L2 cells, dCREB1 activates transcription from CREs, but this effect is not enhanced by cotransfection of PKA (Figure 6). In Kc167 cells, dCREB1 fails to activate reporter expression either alone or with cotransfected PKA expression constructs.

15 Genomic Southern blot analysis indicates that dCREB1 is a single copy gene, and chromosomal *in situ* hybridization shows that it is located at 54A on the right arm of chromosome 2.

These results show that dCREB1 is a non-PKA responsive
20 CREB family member from *Drosophila*.

The following materials and methods were used in the work described in Examples 3 and 4.

Isolating Transgenic Flies

EcoRI restriction sites were added (using PCR) just 5'
25 to the putative translation initiation site and just 3' to the translation termination site in the dCREB2-b cDNA. This fragment was sequenced and subcloned into CaSpeR hs43, a mini-white transformation vector which contains the hsp70 promoter, in the orientation so that the dCREB2-b open
30 reading frame is regulated by the hsp70 promoter. Germ-line transformation was accomplished using standard techniques (Spradling, A.C. and G.M. Rubin, *Science*, 218: 341-347 (1982); Rubin, G.M. and A. Spradling, *Science*, 218:

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348-353 (1982)). Two transgenic lines, 17-2 and M11-1, each with one independent P-element insertion were generated and characterized. They appeared normal in general appearance, fertility and viability. These
5 transgenic lines were outcrossed for at least five generations to w(CS-10) (Dura, J-M., et al., *J. Neurogenet.* 9: 1-14 (1993)), which itself had been outcrossed for ten generations to a wild-type (Can-S) stock. This extensive series of outcrossing is necessary to equilibrate the
10 genetic background to that of Canton-S. Flies homozygous for the 17-2 transgene were bred and used for all experiments.

The mutant blocker has been described previously (see Example 1). The mutations were substituted into an
15 otherwise wild-type blocker construct and germ-line transformants were made by injecting into w(isoCJ1) embryos. Flies homozygous for the A2-2 transgene insertion were bred and used for all experiments. w(isoCJ1) is a subline of w(CS10) (see above) carrying
20 isogenic X, 2nd and 3rd chromosomes and was constructed by Dr. C. Jones in our laboratory. Originally 40 such sublines were w(CS10) using standard chromosome balancer stocks. Olfactory acuity, shock reactivity, learning and three-hr memory after one-cycle training then were assayed
25 in each isogenic subline. As expected, a range of scores among the sublines was obtained. w(isoCJ1) yielded scores that were most like those of w(CS10) on each of these assays. By injecting DNA into the relatively homogeneous genetic background of w(isoCJ1), outcrossing of the
30 resulting germ-line transformants to equilibrate heterogeneous genetic backgrounds was not necessary.

Cycloheximide Feeding and Heat-Shock Regimen

For experiments on memory retention after one-cycle training and on retrograde amnesia, flies were fed 35 mM

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cycloheximide (+CMX; Sigma) in 4% sucrose (w/v) or 4% sucrose alone (-CXM) at 25°C. Groups of 100 flies were placed in feeding tubes (Falcon 2017) containing two 1.0 x 2.5 cm Whatmann 3MM filter paper strips that were soaked
5 with a total of 250 μ l of solution.

For experiments on one day retention after massed or spaced training, flies were fed 35 mM CXM and (w/v) 5% glucose dissolved in 3% ethanol. Groups of 100 flies were placed in feeding tubes (Falcon 2017) containing one 1.0 x
10 2.5 cm Whatmann 3MM filter paper strips that was soaked with a total of 126 μ l of solution.

For experiments on learning after one-cycle training, olfactory acuity, and shock reactivity, flies were fed a 5% glucose, 3% ethanol solution alone or 35 mM CXM in the
15 glucose/ethanol solution.

The feeding period was limited to 12-14 hrs prior to training, or to the 24-hr retention interval after training. Flies which were fed prior to training were transferred directly to the training apparatus after
20 feeding, subjected to massed or spaced training, then transferred to test tubes containing filter paper strips soaked with 5% glucose during the 24-hr interval. Flies which were fed after training were trained, then transferred immediately to test tubes containing filter
25 paper strips soaked with 5% glucose solution which was laced with 35 mM CXM. Flies remained in the test tubes for the duration of the 24-hr retention interval.

For heat-shock induction, flies were collected within two days of eclosion, placed in glass bottles in groups of
30 about 600, and incubated overnight at 25° C and 70% relative humidity. The next day, three hours before training, groups of approximately 100 flies were transferred to foam-stoppered glass shell vials containing a strip of filter paper to absorb excess moisture. The
35 vials then were submerged in a 37°C water bath until the

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bottom of the foam stopper (inside the vial) was below the surface of the water, thereby insuring that the flies could not escape heat-shock. The vial remained submerged for 30 min, after which the flies were transferred to a standard food vial for a 3-hr recovery period at 25° C and 70% relative humidity. Training began immediately after the recovery period.

Pavlovian Learning and Memory and Testing

Flies were trained with an automated version of the learning procedure of Tully, T. and W.G. Quinn, *J. Comp. Physiol.*, 157: 263-277 (1985). In brief, flies were trapped in a training chamber, the inside of which was covered with an electrifiable copper grid. Groups of about 100 flies were exposed sequentially to two odors [either octanol (OCT) or methylcyclohexanol (MCH)], which were carried through the training chamber in a current of air, for 60 seconds with 45 seconds rest intervals after each odor presentation. During exposure to the first odor, flies also were subjected to twelve 1.5-second pulses of 60 V DC with a 5-second interpulse interval. After training, flies were transferred to food vials for a particular retention interval. Conditioned odor-avoidance responses then were tested by transferring flies to the choice point of a T-maze, where they were exposed simultaneously to OCT and MCH carried in the distal ends of the T-maze arms and out the choice point on converging currents of air. Flies were allowed to distribute themselves in the T-maze arms for two minutes, after which they were trapped in their respective arms, anesthetized and counted. The "percent correct" then was calculated as the number of flies avoiding the shock-paired odor (they were in the opposite T-maze arm) divided by the total number of flies in both arms. (The number of flies left at the choice point, which usually was less than 5%, were not included in this calculation). Finally, a

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performance index (PI) was calculated by averaging the percent corrects of two reciprocal groups of flies -- one where OCT and shock were paired, the other where MCH and shock were paired -- and then by normalizing the average so that a PI=0 represented a 50:50 distribution in the T-maze and a PI=100 represented 100% avoidance of the shock-paired odor. For these studies, three different training protocols were used: 1. One-cycle training consisted of the training session just described. 2. Massed training consisted of 10 of these training cycles delivered one right after the other. 3. Spaced training consisted of 10 training cycles with a 15-min rest interval between each. One-cycle training was used to assay learning, while massed and spaced was used to assay consolidated memories.

15 Olfactory Acuity and Shock Reactivity

Odor avoidance responses to OCT or to MCH at two different concentrations -- one (10^0) usually used in conditioning experiments and a 100-fold (10^{-2}) dilution thereof -- were quantified in various groups of flies in the absence of heat shock and 3 hr or 24 hr after heat shock with the method of Boynton, S. and T. Tully, *Genetics*, 131: 655-672 (1992). Briefly, flies are placed in a T-maze and given a choice between an odor and air. The odors are naturally aversive, and flies ususally choose air and avoid the T-maze arm containing the odor. For shock reactivity, flies are given a choice between an electrified grid in one T-maze arm, and an unconnected grid in the other. After the flies have distributed themselves, they are anesthetized, counted and a PI is calculated.

30 Statistical Analyses of Behavioral Data

Since each PI is an average of two percentages, the Central Limit Theorem predicts that they should be distributed normally (see Sokal, R.R. and F.J. Rohlf,

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Biometry, 2nd Edition, W.H. Freeman and Company, New York (1981)). This expectation was shown to be true by an empirical determination with data from Tully, T. and W.G. Quinn, *J. Comp. Physiol.*, 157: 263-277 (1985) and Tully, T. and D. Gold, *J. Neurogenet.*, 9: 55-71 (1993). Thus, untransformed (raw) data were analyzed parametrically with JMP2.1 statistical software (SAS Institute Inc., Cary NC). Since preliminary experiments preceded all of the experiments summarized herein, all pairwise comparisons were planned. To maintain an experimentwise error rate of $\alpha = 0.05$, the critical P values for these individual comparisons were adjusted accordingly (Sokal, R.R. and F.J. Rohlf, *Biometry*, 2nd Edition, W.H. Freeman and Company, New York (1981)) and are listed below for each experiment.

All experiments were designed in a balanced fashion with N=2 PIs per group collected per day; then replicated days were added to generate final Ns. In each experiment, the experimenter (M.D.) was blind to genotype.

A. One-day memory in wild-type flies fed CXM before or immediately after massed or spaced training (Figure 8): PIs from these four drug treatments (-CXM before, -CXM after, +CXM before and +CXM after) and two training procedures (massed and spaced) were subjected to a TWO-WAY ANOVA with DRUG ($F_{(3,56)} = 8.93$; $P < 0.001$) and TRAINING ($F_{(1,56)} = 18.10$, $P < 0.001$) as main effects and DRUG x TRAIN ($F_{(3,56)} = 4.68$, $P = 0.006$) as the interaction term. P values from subsequent planned comparisons are summarized in Figure 8. The six planned comparisons were judged significant if $P \leq 0.01$.

B. One-day memory after massed or spaced training in dCREB2-b transgenic flies (Figures 9A and 9B): In experiments with the 17-2 transgenic line, PIs from two strains (Can-S and 17-2) and four training-regimens

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(spaced-hs, spaced+hs, massed-hs and massed+hs) were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(1,40)} = 1.57$; $P = 0.22$) and TRAINING-regimen ($F_{(3,40)} = 25.81$, $P < 0.001$) as main effects and STRAIN x TRAIN ($F_{(3,40)} = 6.62$, $P = 0.001$) as the interaction term. A similar analysis was done with data from the M11-1 transgenic line, yielding STRAIN ($F_{(1,40)} = 2.81$; $P = 0.10$), TRAINING-regimen ($F_{(3,40)} = 11.97$, $P < 0.001$) and STRAIN x TRAIN ($F_{(3,40)} = 3.37$, $P = 0.03$) effects. P values from subsequent planned comparisons are summarized in Figures 9A and 9B. In each experiment, the seven planned comparisons were judged significant if $P \leq 0.01$.

C. Learning after one-cycle training in 17-2 transgenic flies (Figure 9C): PIs from two strains (Can-S and 17-2) and three heat-shock regimens [-hs, +hs (3 hr) and +hs (24 hr)] were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(1,30)} = 0.69$; $P = 0.41$) and HEAT-shock regimen ($F_{(2,30)} = 10.29$, $P < 0.001$) as main effects and STRAIN x HEAT ($F_{(2,30)} = 0.71$, $P = 0.50$) as the interaction term. P values from subsequent planned comparisons are summarized in Figure 9C. The three planned comparisons were judged significant if $P \leq 0.02$.

D. One-day memory after spaced training in A2-2 transgenic flies (Figure 10): PIs from these three strains [w(isoCJ1), 17-2 and A2-2] and two heat-shock regimens [-hs and +hs (3 hr)] were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(2,30)} = 9.43$, $P < 0.001$) and HEAT-shock regimen ($F_{(1,30)} = 9.84$, $P = 0.004$) as main effects and STRAIN x HEAT ($F_{(2,30)} = 5.71$, $P = 0.008$) as the interaction term. P values from subsequent comparisons are summarized in Figure 10. The six planned comparisons were judged significant if $P \leq 0.01$.

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E. Olfactory acuity in 17-2 flies (Table): PIs from these two strains (Can-S and 17-2), four different odor-levels (OCT- 10^0 , OCT- 10^{-2} , MCH- 10^0 and MCH- 10^{-2}) and three heat-shock regimens [-hs. +hs (3 hr) and +hs (24 hr)] were subjected to a THREE-WAY ANOVA with STRAIN ($F_{(1,184)} = 0.12$, $P = 0.73$), ODOR-level ($F_{(3,184)} = 126.77$, $P < 0.001$) and HEAT-shock regimen ($F_{(2,184)} = 3.55$, $P = 0.03$) as main effects, STRAIN x ODOR ($F_{(3,184)} = 1.23$, $P = 0.30$), STRAIN x HEAT ($F_{(2,184)} = 0.33$, $P = 0.72$) and ODOR x HEAT ($F_{(6,184)} = 3.14$, $P = 0.006$) as two-way interaction terms and STRAIN x ODOR x HEAT ($F_{(6,184)} = 0.48$, $P = 0.83$) as the three-way interaction term. P values from subsequent planned comparisons are summarized in the Table. The twelve planned comparisons were significant if $P \leq 0.005$.

F. Shock reactivity in 17-2 flies (Table): PIs from these two strains (Can-S and 17-2), two shock groups (60V and 20V) and three heat-shock regimens [-hs, +hs (3 hr) and +hs (24 hr)] were subjected to a THREE-WAY ANOVA with STRAIN ($F_{(1,84)} = 0.50$, $P = 0.48$), SHOCK ($F_{(1,84)} = 97.78$, $P < 0.001$) and HEAT-shock regimen ($F_{(2,84)} = 3.36$, $P = 0.04$) as main effects, STRAIN x SHOCK ($F_{(1,84)} = 1.12$, $P = 0.29$), STRAIN x HEAT ($F_{(2,84)} = 1.06$, $P = 0.35$) and SHOCK x HEAT ($F_{(2,84)} = 6.66$, $P = 0.002$) as two-way interaction terms and STRAIN x SHOCK x HEAT ($F_{(2,84)} = 1.75$, $P = 0.18$) as the three-way interaction term. P values from subsequent planned comparisons are summarized in the Table. The six planned comparisons were judged significant if $P \leq 0.01$.

G. Seven-day memory after spaced training in 17-2 flies (Figure 11): PIs from two strains (Can-S and 17-2) and two heat-shock regimens [-hs and +hs(3 hr)] were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(1,20)} = 6.09$; $P = 0.02$) and HEAT-shock regimen ($F_{(1,20)} = 16.30$, $P = 0.001$) as main effects and STRAIN x TRAIN ($F_{(1,20)} = 7.73$, $P = 0.01$) as

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the interaction term. P values from subsequent planned comparisons are summarized in Figure 11. The three planned comparisons were judged significant if $P \leq 0.02$.

H. One-day memory after spaced training in *rsh;17-2* double mutants (Figure 12): PIs from three strains (17-2, *rsh* and *rsh;17-2*) and two heat-shock regimens [-hs and +hs (3 hr)] were subjected to a TWO WAY ANOVA with STRAIN ($F_{(2,30)} = 32.05$; $P < 0.001$) and HEAT-shock regimen ($F_{(1,30)} = 59.68$, $P < 0.001$) as main effects and STRAIN x TRAIN ($F_{(2,30)} = 11.59$, $P < 0.001$) as the interaction term. P values from subsequent planned comparisons are summarized in Figure 12. The five planned comparisons were judged significant if $P \leq 0.01$.

I. Learning after one-cycle training in *rsh;17-2* mutants (see text): PIs from these two strains (Can-S and *rsh;17-2*) and two heat-shock regimens [-hs and +hs (3 hr)] were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(1,20)} = 86.85$, $P < 0.001$) and HEAT-shock regimen ($F_{(1,20)} = 0.02$, $P < 0.89$) as main effects and STRAIN x HEAT ($F_{(1,20)} = 0.86$, $P = 0.37$) as the interaction term. P values from subsequent planned comparisons are summarized in the Table. The two planned comparisons were significant if $P \leq 0.03$.

J. Olfactory acuity in *rsh;17-2* flies (Table): PIs from these two strains (Can-S and *rsh;17-2*), four different odor-levels (OCT- 10^0 , OCT- 10^{-2} , MCH- 10^0 and MCH- 10^{-2}) and two heat-shock regimens [-hs, and +hs (3 hr)] were subjected to a THREE-WAY ANOVA with STRAIN ($F_{(1,112)} = 0.02$, $P = 0.88$), ODOR-level ($F_{(3,112)} = 50.03$, $P < 0.001$) and HEAT-shock regimen ($F_{(1,112)} = 29.86$, $P < 0.001$) as main effects, STRAIN x ODOR ($F_{(3,112)} = 2.15$, $P = 0.10$), STRAIN x HEAT ($F_{(1,112)} = 0.34$, $P = 0.56$) and ODOR x HEAT ($F_{(3,112)} = 6.41$, $P = 0.001$) as two-way interaction terms and STRAIN x ODOR x HEAT

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($F_{(3,112)} = 1.12$, $P = 0.35$) as the three-way interaction term. P values from subsequent planned comparisons are summarized in the Table. The eight planned comparisons were judged significant if $P \leq 0.01$.

- 5 K. Shock reactivity in *rsh;17-2* flies (Table): PIs from these two strains (Can-S and *rsh;17-2*), two shock groups (60V and 20V) and two heat-shock regimens [-hs and +hs (3 hr)] were subjected to THREE-WAY ANOVA with STRAIN ($F_{(1,56)} = 0.51$, $P = 0.48$), SHOCK ($F_{(1,56)} = 88.14$, $P < 0.001$)
10 and HEAT-shock regimen ($F_{(1,56)} = 0.08$, $P = 0.77$) as main effects, STRAIN x SHOCK ($F_{(1,56)} = 0.12$, $P = 0.73$, STRAIN x HEAT ($F_{(1,56)} = 0.03$, $P = 0.86$) and SHOCK x HEAT ($F_{(1,56)} = 0.39$, $P = 0.53$) as two-way interaction terms and STRAIN x SHOCK x HEAT ($F_{(1,84)} = 1.58$, $P = 0.21$) as the three-way
15 interaction term. P values from subsequent planned comparisons are summarized in the Table. The four planned comparisons were judged significant if $P \leq 0.01$.

Northern Analysis

- For RNA collection, the heat-shock regimen was the
20 same as for behavioral experiments. For any indicated time interval between heat-shock and collection, flies rested in food-containing vials at 25°C. Flies were collected and quickly frozen in liquid nitrogen. All Northern analyses used head RNA. The tube of frozen flies was repeatedly
25 rapped sharply on a hard surface, causing the heads to fall off. The detached frozen heads were recovered by sieving on dry ice. Approximately 1000 heads were pooled for RNA preparation. Wild-type and transgenic flies for each individual time point always were processed in parallel.
30 Flies that were not induced were handled in a similar manner to induced flies, except that the vials were not placed at 37°C. Total head RNA was isolated from each group of flies, and poly A+ RNA was isolated using oligo dT

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columns according to the instructions of the manufacturer (5'--->3' Inc.). The concentration of poly A+ mRNA was measured spectrophotometrically, and 0.5 mg of mRNA per lane was loaded and run on 1.2% formaldehyde-agarose gels.

5 Northern blots were prepared, probed and washed (0.1 x SSC at 65°C) as described (Ausubel, F., *Current Protocols in Molecular Biology*, John Wiley and Sons, New York, 1994). For detection of the transgene, an 843bp dCREB2-b cDNA fragment was subcloned into pKS+ and used to generate a

10 uniformly-labeled antisense riboprobe. This fragment codes for the carboxyl-terminal 86 amino acids of the dCREB2-b protein plus 3' untranslated mRNA.

Western Blot Analysis and Antiserum

Western blot analysis was performed using a rabbit

15 antiserum raised against a peptide corresponding to 16 amino acids in the basic region of the dCREB2-b cDNA with an additional COOH terminal Cys. The sequence of the peptide was: (SEQ ID NO.: 24) NH₂-RKREIRLQKNREAAREC-COOH. The peptide was synthesized and coupled to Sulfo-SMCC

20 (Pierce) activated keyhole limpet hemocyanin. The antigen was injected into rabbits (100 µg) and boosted at two week intervals. Sera was bled and tested for immune reactivity towards bacterially-expressed dCREB2-b protein. The antiserum was passed through a CM Affi-gel Blue column

25 (Biorad), and the flow-through was concentrated by ammonium sulfate precipitation, resuspended and dialyzed against PBS (0.14 M NaCl, 2.7 mM KCl, 4.3 mM Na₂HPO₄·7H₂O, 1.4 mM KH₂PO₄, pH 7.3). The dialyzed serum was affinity-purified using a peptide column made using an Ag/Ab Immobilization kit

30 (Immunopure from Pierce). After the antiserum was eluted using a 4M MgCl₂, 0.1 M HEPES pH 6.0 buffer, it was dialyzed into PBS and frozen.

Each data point represents approximately 5 fly heads. Groups of about 25-50 flies were collected and quickly

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frozen on liquid nitrogen until all of the time points had been collected. Heads were isolated resuspended in approximately 200 μ l of 1x Laemmli sample buffer, allowed to thaw and homogenized with a Dounce type B pestle.

- 5 Samples were boiled for 5 minutes, and centrifuged for 10 minutes at room temperature in an Eppendoff microcentrifuge. The supernatants were collected and boiled again just prior to loading onto protein gels. Standard procedures were used to separate equal amounts of
- 10 proteins from each sample on 12% polyacrylamide-SDS gels and to transfer them to PVDF membranes by electroblotting (Ausubel, F., *Current Protocols in Molecular Biology*, John Wiley and Sons, New York, 1994).

- The membranes were blocked for 60 minutes with a 5% BSA solution made up in TBST (10 mM Tris, pH 7.9, 150 mM NaCl, 0.05% Tween 20). The primary antibody was diluted 1:1000 in TBST and incubated with the filter for 30 minutes. The membranes were washed three times with TBST for 5 minutes each time and then incubated for 30 minutes
- 20 with an alkaline phosphatase-conjugated anti-rabbit IgG second antibody (Promega) diluted 1:7500 in TBST. The membranes were washed three more times as before and developed using a chromogenic alkaline phosphatase reaction according to manufacturers suggestions (Promega).

25 Example 3 Transgene Expression Increased After Heat-Shock Induction

- In order to interpret the effects of transgene induction on behavior, dCREB2-b expression in transgenic flies (17-2) after heat-shock induction was measured.
- 30 Northern blot analysis revealed elevated levels of hs-dCREB2-b message in the 17-2 flies immediately and three hours after heat-shock (Figure 7A). This induction was also detectable in brain cells using *in situ* hybridization. Western blot showed increased dCREB2-b protein immediately

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after induction (Figure 7B). Elevated levels of the dCREB2-b protein were seen nine hours later and were still detectable twenty four hours after induction. These data indicate that increased amounts of dCREB2-b existed in
5 brain cells throughout spaced training, which ended about six hours after heat induction.

The behavioral experiments also used transgenic flies (A2-2) which expressed a mutated dCREB2-b protein (dCREB2-mLZ). These mutations changed the two internal
10 leucine residues of the leucine zipper to valine residues, and these changes have been shown to result in a protein which is unable to form dimers (Dwarki, V.J. et al., *EMBO J.*, 9: 225-232 (1990)). In transient co-transfection assays, the mutant protein was unable to block
15 PKA-dependent transcription mediated by dCREB2-a, while the wild-type protein had blocking function. Western blot analysis showed that the wild-type and mutant blocker are expressed at similar levels beginning immediately after heat-shock induction and lasting for at least 6 hours
20 (Figure 7C). Therefore, it is unlikely that these two proteins have large differences in expression levels or stability in the transgenic flies.

Northern blot analysis of two different housekeeping genes, myosin light chain (Parker, V.P., et al., *Mol. Cell Biol.*, 5: 3058-3068 (1985)) and elongation factor α
25 (Hovemann, B., et al., *Nucleic Acids Res.*, 16: 3175-3194 (1988)), showed that steady-state levels of their RNAs were unaffected after transgene induction for at least 3 hours. Gel shift analysis using two different consensus DNA
30 binding sites showed that there was no large effect on the gel shift species which formed after transgene induction for at least 9 hours. Cotransfection of the blocker did not interfere with the activity of a transcription factor from a different family in cell culture. Considered

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together, *hs-dCREB2-b* probably had fairly specific molecular modes of action after induction.

Example 4 Assessment of the Role of CREBs in Long-Term Memory Formation

5 Flies were fed 35 mM cycloheximide (CXM) for 12-14 hours before, or for the 24-hr retention interval immediately after, massed or spaced training (Figure 8). Each of these CXM feeding regimens significantly reduced one-day memory after spaced training but had no effect on
10 one-day memory after massed training (Figure 8). Thus, cycloheximide feeding immediately before or after spaced training disrupts one-day memory. These results suggest that protein synthesis is required soon after training for the formation of long-lasting memory.

15 The results in Figure 8 show that cycloheximide feeding affects one-day retention after spaced training but not massed training. Different groups of wild-type (Can-S) flies were fed 5% glucose solution alone (hatched bars) or laced with 35 mM CXM (striped bars) either for 12-14 hr
20 overnight before massed or spaced training or for the 24-hr retention interval immediately after training. One-day memory retention was significantly lower than normal in flies fed CXM before ($P < 0.001$) or after ($P < 0.001$) spaced training. In both cases, one-day retention in CXM-
25 fed flies was reduced to a level similar to one-day memory after massed training in glucose-fed flies ($P = 0.88$ for CXM before training and $P = 0.71$ for CXM after training). In contrast, no difference was detected between CXM-fed and control flies for one-day memory after massed training ($P =$
30 0.49 and $P = 0.46$, respectively).

One day retention after spaced training was unaffected in uninduced (-hs) transgenic flies (17-2) but was significantly reduced in induced (+hs) transgenic flies (Figure 9A). In contrast, one-day retention after massed

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training was normal in both uninduced and induced transgenic flies (Figure 9A). Comparisons of one-day retention after spaced or massed training between wild-type flies with (+hs) or without (-hs) heat-shock indicated that the heat-shock regimen itself did not have a non-specific effect on memory after either training protocol. Thus induction of the *dCREB2-b* transgene only affected (i.e., disrupted) one-day memory after spaced training.

One day retention after spaced or massed training in *M11-1*, a second line carrying an independent *hs-dCREB2-b* insertion, also was tested. Results with *M11-1* were similar to those obtained with *17-2* (Figure 9B). These results show that the effect of induced *hs-dCREB2-b* does not depend on any particular insertion site of the transgene.

The results in Figures 9A-9C show that induction of the *dCREB2-b* transgene disrupts one-day memory after spaced training, while one-day memory after massed training and learning are normal.

In Figure 9A, different groups of wild-type (Can-S) flies (hatched bars) or *hs-dCREB2-b* transgenic (*17-2*) flies (striped bars) were given spaced training or massed training in the absence of heat shock (-hs) or three hours after heat shock (+hs). After training, flies were transferred to standard food vials and stored at 18°C until one-day memory was assayed. No differences in one-day memory after spaced or massed training were detected between Can-S vs. *17-2* flies in the absence of heat shock (-hs; $P = 0.83$ and 0.63 , respectively). When flies were trained three hours after heat shock (+hs), however, one-day memory was significantly different between Can-S v. *17-2* flies after spaced training ($P < 0.001$) but not after massed training ($P = 0.23$). In fact, the one-day memory after spaced training was no different than that after massed training in induced *17-2* flies ($P = 0.59$). In

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addition, the heat-shock regimen did not produce a non-specific effect on one-day retention after spaced ($P = 0.59$) or massed ($P = 1.00$) training in Can-S flies. $N=6$ performance indices (PIs) per group.

5 The experiment described in Figure 9A was repeated in Figure 9B with a second, independently derived *dCREB2-b* transgenic line, *M11-1* (striped bars). Here again, a) no differences in one-day memory after spaced or massed training were detected between Can-S vs. *M11-1* flies in the
10 absence of heat-shock (-hs; $P = 0.83$ and 0.86 , respectively), b) a significant difference between Can-S v. *M11-1* for one-day memory after spaced training ($P < 0.001$) but not after massed training ($P = 0.85$) when trained three hours after heat-shock (+hs), c) one-day memory after
15 spaced training was no different than that after massed training in induced *M11-1* flies ($P = 0.43$) and d) the heat-shock regimen did not produce a non-specific effect on one-day retention after spaced ($P = 0.59$) or massed ($P = 0.94$) training in Can-S flies. $N=6$ PIs per group.

20 If induction of the transgene specifically affected LTM via disruption of gene expression, then learning should not be affected, since it does not require new protein synthesis. Different groups of flies were trained using one-cycle training either without heat-shock, or three or
25 twenty four hours after heat-shock. These time points after induction were selected to correspond to the times when flies were trained and tested in the previous experiments (see Figures 9A and 9B). Induction of the transgene (*d-CREB2-b*) in the 17-2 line had no effect on
30 learning in either case (Figure 9C).

 In Figure 9C, different groups of Can-S flies (hatched bars) or 17-2 transgenic flies (striped bars) received one-cycle training in the absence of heat shock (-hs) or three (+hs 3hr) or 24 (+hs 24hr) hours after heat-shock and then
35 were tested immediately afterwards. In each case, no

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differences between Can-S vs. 17-2 flies were detected (P s = 0.28, 0.64 and 0.42, respectively), indicating that learning was normal in induced or uninduced transgenic flies. $N=6$ PIs per group.

5 Induction of the transgene which contained the mutant blocker (A2-2) did not affect one-day retention after spaced training, while the wild-type blocker (17-2) had a dramatic effect (Figure 10). The *w(iso CJ1)* flies, whose one-day retention also was unaffected by heat induction, is
10 the isogenic control for the mutant blocker transgenic flies. Since Western blot analysis showed that wild-type and mutant blockers probably have similar expression levels, this result suggests that the blocker requires an intact leucine zipper to function effectively.

15 Figure 10 shows that induction of the *hs-dCREB2-mLZ* mutant blocker does not affect one-day retention after spaced training. Different groups of wild-type [*w(iso CJ1)*], *hs-dCREB2-b* transgenic (17-2) or mutant *hs-dCREB2-mLZ* transgenic flies (A2-2) received spaced training in the
20 absence of heat-shock (-hs) or three hours after heat-shock (+hs). The flies were then handled and tested as in Figure 9A. No differences in one-day memory after spaced training were detected between *w(isoCJ1)* vs. 17-2 flies or between
25 *w(isoCJ1)* vs. A2-2 flies in the absence of heat shock (-hs; $P = 0.38$ and 0.59 , respectively). When flies were trained three hours after heat shock (+hs), however, one-day memory after spaced training was significantly different between
30 *w(isoCJ1)* vs. 17-2 flies ($P < 0.001$) -- as in Figure 9A -- but was not different between *w(isoCJ1)* vs. A2-2 flies ($P = 0.78$). In addition, the heat-shock regimen did not produce a non-specific effect on one-day retention after spaced training in *w(isoCJ1)* or A2-2 flies ($P = 0.40$ and $P = 0.97$, respectively. $N=6$ performance indices (PIs) per group.

Olfactory acuity and shock reactivity are component
35 behaviors essential for flies to properly learn odor-shock

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associations. The Table shows the scores for these peripheral behaviors for Can-S versus 17-2 flies. With or without heat-shock, olfactory acuity and shock reactivity were normal in 17-2 transgenic flies. Thus, *hs-dCREB2-b* induction does not affect olfactory acuity or shock reactivity.

If induction of *hs-dCREB2-b* blocks long-term memory (LTM), then long-lasting memory also should be blocked. In wild-type flies, seven-day retention after spaced training consists solely of the CXM-sensitive LTM because the CXM insensitive ARM component has decayed away. In uninduced transgenic flies (17-2), seven-day retention after spaced training was similar to retention in uninduced wild-type flies ($P = 0.83$; Figure 11). Seven-day retention was severely disrupted, however, in transgenic flies which were trained three hours after heat-shock ($P = 0.001$) and did not differ from zero ($P = 0.91$). In contrast, the heat-shock protocol had no detectable effect on seven-day memory in wild-type flies ($P = 0.39$). Thus, induction of *hs-dCREB2-b* disrupts long-term memory (LTM).

Figure 11 shows that induction of *hs-dCREB2-b* completely abolishes 7-day memory retention. Previous analyses of *radish* mutants indicated that memory retention four or more days after spaced training reflects the sole presence of LTM. Thus, the effect of induced *hs-dCREB2-b* on LTM was verified by comparing 7-day retention after spaced training in Can-S (hatched bars) vs. 17-2 transgenic (striped bars) flies that were trained in the absence of heat-shock (-hs) or three hours after heat shock (+hs). Flies were stored in standard food vials at 18°C during the retention interval. $N=6$ PIs per group. Seven-day retention after spaced training did not differ between Can-S and 17-2 in the absence of heat-shock ($P = 0.83$) but was significantly lower than normal in 17-2 flies after heat-shock ($P = 0.002$). In fact, 7-day retention after spaced

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training in induced 17-2 transgenic flies was not different from zero ($P = 0.92$). In addition, the heat-shock regimen did not affect 7-day retention after spaced training non-specifically in Can-S flies ($P = 0.39$).

5 If induction of the *hs-dCREB2-b* transgene specifically blocks LTM, then it should only affect the CXM-sensitive component of consolidated memory after spaced training. For both transgenic lines, 17-2 and M11-1, the effect of transgene induction looked similar to the effect that CXM
10 had on wild-type flies (compare Figure 8 with Figures 9A and 9B). This similarity suggested that the induced dCREB2-b protein completely blocked CXM-sensitive memory, leaving ARM intact. The *radish* mutation disrupts ARM (Folkers, E., et al., *Proc.Natl.Acad.Sci. USA*, 90: 8123-
15 8127 (1993)), leaving only LTM one day after spaced training. Thus, a *radish hs-dCREB2-b* "double mutant" (*rsh*; 17-2) was constructed to allow examination of LTM in the absence of ARM. In the absence of heat-shock, *rsh*;17-2 double-mutants and *radish* single-gene mutants yielded
20 equivalent one-day retention after spaced training (Figure 12). In contrast, when these flies were heat-shocked three hours before spaced training, one-day retention was undetectable in *rsh*;17-2 flies but remained at mutant levels in *radish* flies. The double mutant also showed
25 normal (*radish*-like) learning ($P = 0.59$) and normal (wild-type) olfactory acuity and shock reactivity in the absence of heat-shock versus three hours after heat shock (see the Table).

Figure 12 shows that induction of *hs-dCREB2-b*
30 completely abolishes one-day memory after spaced training in *radish*; 17-2 "double mutants." Since *radish* is known to disrupt ARM, a clear view of the effect of *hs-dCREB2-b* on LTM was obtained in *radish*;17-2 flies. One-day retention after spaced training was assayed in *rsh*;17-2 double
35 mutants and in 17-2 and *rsh* single-gene mutants as

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controls. Flies were trained in the absence of heat-shock (hatched bars) or three hours after heat-shock (striped bars) and stored at 18°C during the retention interval. As usual, induction of *hs-dCREB2-b* produced significantly
5 lower one-day memory after spaced training in 17-2 flies ($P < 0.001$). The heat-shock regimen, however, had no effect on such memory in *radish* mutants

TABLE 1. Olfactory acuity and shock reactivity in Can-S (wild-type), 17-2 (*hs-dCREB2-b* transgenic) and *rsh*; 17-2 (*radish*, *hs-dCREB2-b* "double mutant") flies^a.

Heat Shock	Group	Olfactory Acuity				Shock Reactivity	
		OCT		MCH		60V	20V
		10 ⁰ *	10 ⁻²	10 ⁰	10 ⁻²		
-hs	CAN-S 17-2	58±3 60±3	32±3 34±8	80±2 77±3	33±7 37±5	79±5 87±3	52±5 43±2
+hs (3 hrs)	CAN-S 17-2	69±4 71±4	41±4 37±3	77±2 76±5	25±9 26±3	74±5 78±3	58±6 67±5
+hs (24 hr)	CAN-S 17-2	66±2 65±3	56±8 42±6	79±4 76±3	33±2 41±5	84±3 85±2	63±3 60±6
-hs	CAN-S <i>rsh</i> ; 17-2	51±4 57±3	39±5 39±5	72±5 74±5	33±7 29±4	87±3 82±4	52±5 53±6
+hs (3 hr)	CAN-S <i>rsh</i> ; 17-2	72±4 68±4	48±3 46±6	66±2 78±2	60±3 49±4	80±4 83±1	58±6 50±5

^a Olfactory acuity and shock reactivity were assayed in untrained flies with the methods of Boynton, S. and T. Tully, *Genetics*, 131: 655-672 (1992) and Dura, J-M., et al., *J. Neurogenet.*, 9: 1-14 (1993), respectively (see Examples for more details). N=98 Fls per group.

Planned comparisons between Can-S vs. mutant flies failed to detect any significant differences with any heat-shock regimen.

*10⁰ is manual concentration and corresponds to 10⁻³ for bubbler.

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($P = 0.52$), which reflects only the presence of LTM. In contrast, heat-shock produced significantly lower scores in *rash;17-2* double mutants ($P < 0.001$), which were not different from zero ($P = 0.20$). $N=6$ PIs per group.

5

The following materials and methods were used in the work described in Examples 5 and 6.

Pavlovian Learning and Memory and Testing

10 During one training session, a group of about 100 flies was exposed sequentially to two odors [either octanol (OCT) or methylcyclohexanol (MCH)] for 60 seconds with 45-second rest intervals after each odor presentation. During exposure to the first odor, flies received twelve 1.5-
15 second pulses of 60 V DC with a 5-second interpulse interval.

After training, flies were transferred to food vials and stored at 18°C for a seven-day retention interval. Conditioned odor-avoidance responses then were tested by
20 transferring flies to the choice point of a T-maze, where they were exposed simultaneously to OCT and MCH carried on converging currents of air in the distal ends of the T-maze arms and out the choice point.

Flies were allowed to distribute themselves in the T-maze arms for 120s, after which they were trapped in their
25 respective arms, anesthetized and counted. The "percent correct" then was calculated as the number of flies avoiding the shock-paired odor (they were in the opposite T-maze arm) divided by the total number of flies in both
30 arms. (The number of flies left at the choice point, which usually was less than 5%, were not included in this calculation.) Finally, a performance index (PI) was calculated by averaging the percent corrects of two reciprocal groups of flies -- one where OCT and shock were
35 paired, the other where MCH and shock were paired--and then

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by normalizing the average so that a PI=0 represented a 50:50 distribution in the T-maze and a PI=100 represented 100% avoidance of the shock-paired odor.

All behavioral experiments were designed in a balanced fashion with N=2 PIs per group collected per day; then replicated across days to generate final Ns. In all experiments, the experimenter was blind to genotype.

Statistical Analyses of Behavior Data

PIs are distributed normally (Tully, T. and D. Gold, *J. Neurogenet.*, 9: 55-71 (1993)). Consequently, untransformed (raw) data were analyzed parametrically with JMP3.01 statistical software (SAS Institute Inc., Cary NC). Negative accelerating exponential Gompertz (growth) functions (see Lewis, D., *Quantitative Methods in Psychology*, McGraw-Hill, New York, New York (1960)) were fit to the data in Figures 13A and 13B via nonlinear least squares with iteration.

Example 5 Effect on Long Term Memory of Repeated Training Sessions

Seven-day memory retention (a measure of long term memory) in wild-type (Can-S) flies is induced incrementally by repeated training sessions. An automated version of a discriminative classical conditioning procedure was used to electroshock flies during exposure to one odor (CS+) but not to a second odor (CS-). Seven days after one or more training sessions, memory retention of conditioned odor avoidance responses was quantified in a T-maze, where flies were presented the CS+ and CS- simultaneously for 120 seconds.

In Figure 13A, long term memory as a function of the number of training sessions is indicated by open circles. One training session produced a mean performance index (PI \pm SEM; Note 1) near zero. Additional training sessions

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with a 15-minute rest interval between each, however, yielded a steady increase in mean PIs with a maximum of 39 after ten training sessions. Ten additional training sessions produced similar performance. A nonlinear "growth" function (solid line) was fit to the individual PIs using an iterative least squares method. N = 13, 6, 6, 6, 13, 7, 7, 7, 7, 6, 7 and 7 PIs for groups receiving 1-10, 15 and 20 training sessions, respectively.

10 Example 6 Effect on Long Term Memory of the Rest Interval Between Each Training Session

Seven-day memory retention (a measure of long term memory) in wild-type (Can-S) flies is induced incrementally by the rest interval between each training session. As described in Example 5, an automated version of a discriminative classical conditioning procedure was used to electroshock flies during exposure to one odor (CS+) but not to a second odor (CS-). Seven days after one or more training sessions, memory retention of conditioned odor avoidance responses was quantified in a T-maze, where flies were presented the CS+ and CS- simultaneously for 120 seconds.

In Figure 13B, long term memory as a function of the rest interval is indicated by open circles. Ten training sessions with no rest interval between each (massed training) produced a mean PI near zero. Increasing the rest interval between each of ten training sessions yielded a steady increase in mean PIs with a maximum of 34 for a 10-minute rest interval. Rest intervals up to ten minutes longer produced similar performance. A nonlinear growth function (solid line) was fit to the data as above. N = 12, 6, 6, 6, 6, 13, 7, 7, 7, 7, 7, 7 and 7 PIs for groups receiving 0-10, 15 and 20 minutes of rest between each training session.

35

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The following materials and methods were used in the work described in Examples 7-10.

Isolating Transgenic Flies

5 EcoRI restriction sites were added (using PCR) just 5' to the putative translation initiation site and just 3' to the translation termination site in the *dCREB2-a* cDNA. This fragment was sequenced and subcloned into CaSpeR hs43, a mini-white transformation vector which contains the *hsp70* promoter, in the orientation so that the *dCREB2-a* open reading frame is regulated by the *hsp70* promoter. Germ-line transformation was accomplished by injecting into isogenic *w(isoCJ1)* embryos using standard techniques (Spradling, A.C. and G.M. Rubin, *Science*, 218: 341-347 (1982); Rubin, G.M. and A. Spradling, *Science*, 218: 348-353 (1982)). By injecting DNA into the relatively homogeneous genetic background of *w(isoCJ1)*, outcrossing of the resulting germ-line transformants to equilibrate (heterogeneous) genetic backgrounds was not necessary. Two transgenic lines, C28 and C30, each with one independent P-element insertion were generated and characterized. They appeared normal in general appearance, fertility and viability. Flies homozygous for the C28 or C30 transgene were bred and used for all experiments.

25

Heat Shock Regimen

For heat-shock induction, flies were collected within two days of eclosion, placed in glass bottles in groups of about 600, and incubated overnight at 25°C and 70% relative humidity. The next day, three hours before training, groups of approximately 100 flies were transferred to foam-stoppered glass shell vials containing a strip of filter paper to absorb excess moisture. The vials then were submerged in a 37°C water bath until the bottom of the foam stopper (inside the vial) was below the surface of the

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water, thereby insuring that the flies could not escape heat-shock. The vial remained submerged for 30 minutes, after which the flies were transferred to a standard food vial for a 3-hr recovery period at 25°C and 70% relative humidity. Training began immediately after the recovery period.

Statistical Analyses of Behavior Data

PIs from the three strains (Can-S, C28 and C30) and six training-regiments (1x+hs, 2xmassed+hs, 10xmassed+hs, 1x-hs, 2xmassed-hs and 10xmassed-hs) were subjected to a TWO-WAY ANOVA with STRAIN ($F_{(2, 102)}=48.34$; $P < 0.001$) and TRAINING-regimen ($F_{(5, 102)}=25.47$, $P < 0.001$) as main effects and STRAIN x TRAIN ($F_{(10, 102)}=5.85$, $P < 0.001$) as the interaction term. Since preliminary experiments preceded all of the experiments summarized herein, all pairwise comparisons were planned. To maintain an experimentwise error rate of $\alpha = 0.05$, the individual comparisons summarized in Figure 15B were judged significant if $P < 0.002$ (Sokal, R.R. and F.J. Rohlf, Biometry, 2nd Edition, W.H. Freeman and Company, New York (1981)).

Example 7 A Molecular Switch for the Formation of Long Term Memory

Figure 14 presents a conceptual method of a molecular switch for the formation of LTM, based on differential regulation of CREB isoforms with opposing functions.

Immediately after one training session, the relevant CREB activators and repressors are induced. Their combined functions (rather than molecular concentrations) are equivalent and yielded no net effect of CREB activators. Thus, repeated sessions of massed training (no rest interval) never induce LTM (see Figure 15A). CREB repressors functionally inactivate faster than CREB activators, however, yielding an increasing net effect of

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CREB activators (ΔC) with time (see Figure 13B). If ΔC is positive at the end of a particular rest interval during spaced training, then CREB activators are free to initiate downstream events involved with the formation of LTM.

- 5 Usually, ΔC after one training session is not large enough to yield much LTM. Thus, repeated spaced training sessions serve to increase ΔC incrementally eventually to produce maximal LTM (see Figure 13A).

10 Experimental verification of two predictions from this model involving CREB as a molecular switch for long term memory formation is shown in Figures 15A-15C and discussed in Examples 8-10.

15 Example 8 Effect on Long Term Memory of Having Equal
Amounts of CREB Activators and Repressors
Immediately After One Training Session

The model of a molecular switch for LTM predicts that the functional effects of all CREB activators and repressors are equal immediately after one training session ($\Delta C=0$). If no rest interval occurred between additional training sessions (massed training), then functional CREB activator would not accumulate, thereby preventing the induction of downstream events required for LTM induction.

20

To test this notion, wild-type (Can-S) flies were subjected to 48, instead of the usual 10 (see Figure 15B), massed training sessions (48x massed) or, as a positive control, to 10 spaced training sessions with a 15-minute rest interval (10x spaced). Seven-day memory after such massed training was near zero (Figure 15A), while that after spaced training was near its usual maximum value (see Figure 13A). Thus, nearly five times the usual amount of massed training still did not induce LTM. N=6 PIs for each group.

25

30

PIs from two groups (10x spaced or 48x massed) of wild-type (Can-S) flies were subjected to a ONE-WAY ANOVA

35

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with GROUP ($F_{(10)}=51.13$; $P < 0.001$) as the main effect. A subsequent planned comparison revealed that the mean PI of the 48x massed group did not differ significantly from zero ($t_{(10)}=1.66$; $P=0.127$).

5

Example 9 Effect on Long Term Memory of Increasing Amounts of CREB Activator

The model of a molecular switch for LTM predicts that experimentally increasing the amount of CREB activator will
10 eliminate the requirements for at least 10 repeated training sessions with a 10-minute rest interval between each to produce maximal LTM.

To test this idea, two transgenic lines (C28 and C30) carrying an inducible *hsp-dCREB2-a* activator construct
15 inserted into different cytological locations were generated. Different groups of flies from these two transgenic lines were subjected, along with wild-type (Can-S) flies, to 1 (1x) 2 (2x) or (10x) massed training sessions three hours after heat-shock induction of the
20 transgene (induced) or in the absence of heat-shock (uninduced).

Without heat-shock, seven-day memory in all three strains did not differ from zero after one, two or ten massed training sessions (all $P_s > 0.002$). With heat-
25 shock, seven-day memory in wild-type flies remained near zero in each massed training group (all $P_s > 0.002$). In contrast, seven-day memory was significant (near the maximum of 35) after ten massed sessions in both the C28 and C30 transgenic lines (all $P_s < 0.0001$). Moreover,
30 seven-day memory after one training session was similar to that after ten training sessions in both C28 ($P = 0.89$) and C30 ($P = 0.89$) transgenic flies. Thus, maximum LTM was induced after just one training session in transgenic flies expressing abnormally high levels of CREB activator. $N=10$,

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4 and 6 PIs for each group of Can-S, C28 and C30, respectively.

Example 10 Olfactory Acuity and Shock Reactivity

5 Odor avoidance responses to OCT or to MCH were quantified with the method of Boynton, S. and T. Tully, *Genetics*, 131: 655-672 (1992), given a choice between an odor and air. The odors are naturally aversive, and flies usually chose air and avoided the T-maze arm containing the
10 odor. After 120 seconds, the flies were trapped in their respective arms of the T-maze, anesthetized and counted. A PI was calculated as a normalized percent correctly avoiding the odor (cf. Example 5). PIs from these two strains and two odor-groups (OCT and MCH) were subjected to
15 a TWO-WAY ANOVA with STRAIN ($F_{(1, 12)}=1.57$, $P=0.23$) and ODOR ($F_{(1, 12)}=0.07$, $P=0.80$) as main effects and DRUGxODOR ($F_{(1, 12)}=0.15$, $P=0.71$) as the interaction term. The two subsequent planned comparisons were judged significant if $P < 0.025$.

20 Shock reactivity was quantified with the method of Dura, J-M., et al., *J. Neurogenet.*, 9: 1-14 (1993) in wild-type (Can-S) flies, or in a transgenic line (C28) carrying an inducible *hsp-dCREB2-a* construct, three hours after a 30-minute heat shock at 37°C. Briefly, flies were placed
25 in a T-maze and given a choice between an electrified grid (60V DC) in one T-maze arm and an unconnected grid in the other. After 120 seconds, the flies were trapped in their respective T-maze arms, anesthetized and counted. A PI was calculated as for olfactory acuity. PIs from these two
30 strains were subjected to a ONE-WAY ANOVA with STRAIN ($F_{(1, 6)}=13.03$, $P=0.01$) as the main effect.

Naive avoidance responses to odors or to shock three hours after heat-shock did not differ between wild-type (Can-S) versus transgenic (C28) flies for the two odorants
35 (MCH and OCT) used for conditioning experiments ($P=0.27$,

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0.55, respectively). N=4 PIs per group. Naive shock avoidance responses three hours after training for transgenic flies were slightly lower than those for wild-flies (P=0.01). N=4 PIs per group.

5

Examples 11-13 pertain to the *Drosophila* nitric oxide synthase work.

10 Example 11 Low Stringency Hybridization to a Phage Library of the *Drosophila* Genome and Screening of *Drosophila* cDNA Library

6x10⁴ plaques of a genomic *Drosophila* λDASH library with the 1.3 kb Bgl II fragment of rat neuronal NOS cDNA (residues 3282-4573) under low stringency conditions of 40% formamide were screened as described in W.M. McGinnis et al., *Nature* 308: 428 (1984). Fifty positive phage were purified and grouped based on inter se hybridization. The contig containing the 2.4R fragment of dNOS was comprised of 15 phage clones. Regions of cross-hybridization to the rat probe were identified, subcloned and three of them were sequenced. The other two did not contain sequences homologous to any protein in the database. A *Drosophila* head cDNA library (a gift from P. Salvaterra) was screened with the 2.4R fragment isolated from phage clone λ8.11 in standard conditions. All phage purification and cloning steps were done with standard methods (J. Sambrook, E.F. Fritsch, T. Maniatis, *Molecular cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989)). cDNA fragments were subcloned into Bluescript (Stratagene) and sequenced on both strands with Sequenase 2.0 (USB).

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Example 12 Activity of *Drosophila* Nitric Oxide Synthase
(dNOS)

The expression construct for activity assays contained dNOS cDNA (with an XbaI site engineered immediately
5 upstream of the ATG codon) cloned into the XbaI and SmaI sites of the pCGN expression vector [M. Tanaka and W. Herr, *Cell*, 60: 375 (1990)]. 293 human kidney cells were transfected with 15µg of the dNOS construct, or vector DNA, and precipitated with calcium phosphate as described in
10 [M.J. Imperiale, L.T. Feldman and J.R. Nevins, *Cell*, 35: 127 (1983)]. Cells were collected 2 days later and protein extracts were prepared as described in [J. Sambrook, E.F. Fritsch, T. Maniatis, *Molecular cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory, Cold Spring Harbor,
15 NY, 1989)].

The fusion protein for raising anti-DNOS antibodies was made by cloning a 0.29 kb Eam1105I-SacI fragment of dNOS cDNA (this fragment codes for 97 N-terminal amino acids of dNOS ORF) into EcoRI site of pGEX-KG [K. Guan and
20 J.E. Dixon, *Anal. Biochem.*, 192: 262 (1991)]. The fusion protein was expressed in BL21 *E. coli* strain and purified over Glutathione-Sepharose columns (Pharmacia) as described in [G.J. Hannon, D. Demetrick, D. Beach, *Genes & Dev.*, 7: 2378 (1993)]. Immunization of rabbits, and serum
25 preparation, was done by Hazleton Research Products, Inc. (Denver). The DNOS protein was detected on Western blots using a 1:500 dilution of rabbit serum, and cross-reacting bands were visualized with anti-rabbit alkaline phosphatase conjugate (Promega) according to the protocol provided.

30 The enzymatic assay was done essentially as described previously (D. Bredt and S. Snyder, *Proc. Natl. Acad. Sci. USA*, 87: 682 (1990)]. A 100 ml reaction mixture containing 25 µl (50-100 µg) of soluble protein extract, 50 mM Hepes pH 7.4, 3 µM FAD, 3µM FMN, 10 µM tetrahydrobiopterin (ICN),
35 1 mM DTT, .8 mM CaCl₂, 1 mM NADPH, 10 µg/ml calmodulin, 2µl

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of [³H]L-arginine (35.7 Ci/mmol, NEN) and 50 mM L-valine in was incubated for 60 minutes at 37°C. The reaction was stopped with 0.5 ml 20 mM Hepes pH 5.5, 2mM EDTA, 2mM EGTA, loaded on 0.5 ml Dowex AG 50WX-8 (Na⁺ form) column and
5 eluted with 3x0.5 ml of the stop buffer. Radioactivity present in the eluent was quantified in a scintillation counter.

Figures 17A-17B show the expression of DNOS enzymatic activity in 293 kidney cells. Figure 17A shows the results
10 of a Western blot analysis of protein extracts from 293 cells transfected with vector alone (lane 293 + vector) or with dNOS cDNA construct (lane 293 + dNOS). 25 µg of soluble protein extracts was resolved on 7.5% polyacrylamide gel, transferred to nitrocellulose membrane
15 and treated with anti-DNOS antibody. The arrow indicates the position of the DNOS protein. Positions of molecular weight markers (in kD) are shown on the left.

Figure 17B shows significant DNOS enzyme activity measured in 293 cell extracts by conversion of ³H-L-
20 arginine to ³H-L-citrulline. Enzymatic activity was detected only in cells transfected with dNOS cDNA construct (groups B-D) and is presented as specific activity (pmol of citrulline/mg/min.). The DNOS activity also was measured in the presence of 1 mM EGTA without exogenous Ca²⁺ or
25 calmodulin (group C), or in the presence of 100 mM L-NAME (group D). N=4 reactions per group.

Example 13 Splicing Pattern of dNOS

Heads and bodies of adult flies were separated on
30 sieves. Total RNA was isolated by the guanidinium isothiocyanate method [P. Chomczynski and N. Sacchi, Anal. Biochem., 162: 156 (1987)]. Poly(A)⁺ RNA selection, Northern blot and hybridization were done with standard methods (J. Sambrook, E.F. Fritsch, T. Maniatis, Molecular
35 cloning: A Laboratory Manual (Cold Spring Harbor

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Laboratory, Cold Spring Harbor, NY, 1989)]. The blot was hybridized with random-primed dNOS cDNA (10^6 cpm/ml), washed in 0.1xSSC and 0.1% SDS at 65°C and exposed to X-ray film for 72 hours. Two 25-mer primers [corresponding to
5 residues 1374-1399 (the top primer) and 1793-1817 (the bottom primer) in the dNOS sequence] were used to amplify fragments of two dNOS splice products. Each RT-PCR reaction contained 30 ng of poly(A)⁺ head RNA. In the first stage (RT), 90 ng of the bottom primer and 5U of rTth
10 polymerase (Perkin-Elmers) were added and the mixture was incubated in the MJ Research Minicycler[®] in the following sequence of conditions: 95°C/1 minute, 67°C/45 seconds, 70°C/13 minutes. The second stage (PCR) was carried out as follows: 94°C/45 seconds, 63°C/45 seconds, 70°C/90 seconds
15 and was repeated for 35 cycles. Products of the reaction were analyzed on a denaturing polyacrylamide (8%) gel. Bands of interest were isolated, reamplified, cloned into pCR1000 (InVitrogen) and sequenced with Sequenase kit (USB).

20 Northern blot analysis of dNOS expression in adult flies shows a 5.0 kb dNOS transcript present in heads (Figure 18A). Each lane contained 10 mg of poly (A)⁺ mRNA isolated from *Drosophila* heads (H) or bodies (B). The Northern blot was hybridized with the dNOS cDNA as
25 described above. Positions of size markers (in kb) are shown on the left. The blot was overprobed with myosin light chain (MLC) (Parker, V.P., Mol. Cell Biol. 5: 3058-3068 (1985)) as a standard for RNA concentration.

Figure 18B shows that the dNOS gene expresses two
30 alternatively spliced mRNA species. RT-PCR reactions were performed on poly(A)⁺ mRNA isolated from *Drosophila* heads and were resolved on 8% polyacrylamide gel. Arrows indicate the positions of DNA fragments of expected sizes: the 444 bp long-form fragment and the 129 bp short-form
35 fragment (lane +RNA). Other bands present in this lane are

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artifacts from heteroduplexes that failed to denature. Poly(A)⁺ mRNA was omitted from the control reaction (lane -RNA), which otherwise was done in identical conditions. Size markers (kb ladder) are shown in the middle lane (KB).

5

Equivalents

Those skilled in the art will know, or be able to ascertain, using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. These and all other equivalents are intended to be encompassed by the following claims.

10

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(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(A) APPLICATION NUMBER: US 08/361,063

-95-

(B) FILING DATE: 21-DEC-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/319,866

(B) FILING DATE: 07-OCT-1994

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1083 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "cdna and PCR analysis"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAC AAC AGC ATC GTC GAG GAG AAC GGC AAC TCG TCG GCG GCA TCG	48
Met Asp Asn Ser Ile Val Glu Glu Asn Gly Asn Ser Ser Ala Ala Ser	
1 5 10 15	
GGC TCC AAT GAC GTG GTC GAT GTC GTT GCC CAA CAG GCG GCG GCA GCG	96
Gly Ser Asn Asp Val Val Asp Val Val Ala Gln Gln Ala Ala Ala Ala	
20 25 30	
GTG GGC GGC GGC GGT GGA GGA GGA GGA GGC GGC GGC GGC GGT GGT AAC	144
Val Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn	
35 40 45	
CCC CAG CAG CAG CAA CAG AAC CCA CAA AGT ACA ACG GCC GGC GGT CCA	192
Pro Gln Gln Gln Gln Gln Asn Pro Gln Ser Thr Thr Ala Gly Gly Pro	
50 55 60	
ACG GGT GCG ACG AAC AAC GCC CAG GGA GGC GGA GTG TCC TCC GTG CTG	240
Thr Gly Ala Thr Asn Asn Ala Gln Gly Gly Gly Val Ser Ser Val Leu	
65 70 75 80	
ACC ACC ACC GCC AAC TGC AAC ATA CAA TAC CCC ATC CAG ACG CTG GCG	288
Thr Thr Thr Ala Asn Cys Asn Ile Gln Tyr Pro Ile Gln Thr Leu Ala	
85 90 95	
CAG CAC GGA CTG CAG GTG AGC ATT TGG GGA CCG GGT GCT TGG TGT CAA	336
Gln His Gly Leu Gln Val Ser Ile Trp Gly Pro Gly Ala Trp Cys Gln	
100 105 110	

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CTG	TCG	AGT	GTC	AGG	TGT	TAC	GGA	TCC	CAG	CCA	GAA	GTG	GCT	ACC	AAG	384
Leu	Ser	Ser	Val	Arg	Cys	Tyr	Gly	Ser	Gln	Pro	Glu	Val	Ala	Thr	Lys	
		115					120					125				
GAT	GTG	CAG	TCC	GTG	ATA	CAG	GCC	AAT	CCC	TCG	GGA	GTG	ATA	CAG	ACA	432
Asp	Val	Gln	Ser	Val	Ile	Gln	Ala	Asn	Pro	Ser	Gly	Val	Ile	Gln	Thr	
	130					135					140					
GCA	GCT	GGA	ACC	CAG	CAG	CAG	CAA	CAG	GCG	CTG	GCC	GCC	GCC	ACA	GCG	480
Ala	Ala	Gly	Thr	Gln	Gln	Gln	Gln	Gln	Ala	Leu	GCC	GCC	GCC	Ala	Ala	
145					150					155					160	
ATG	CAG	AAG	GTG	GTC	TAC	GTG	GCC	AAG	CCG	CCG	AAC	TCG	ACG	GTC	ATC	528
Met	Gln	Lys	Val		Tyr	Val	Ala	Lys	Pro	Pro	Asn	Ser	Thr	Val	Ile	
				165					170					175		
CAC	ACG	ACG	CCT	GGC	AAT	GCA	GTG	CAA	GTG	CGT	AAC	AAA	ATC	CCT	CCA	576
His	Thr	Thr	Pro	Gly	Asn	Ala	Val	Gln	Val	Arg	Asn	Lys	Ile	Pro	Pro	
			180					185					190			
ACC	TTT	CCA	TGT	AAG	ATC	AAG	CCC	GAA	CCG	AAC	ACG	CAG	CAC	CCG	GAG	624
Thr	Phe	Pro	Cys	Lys	Ile	Lys	Pro	Glu	Pro	Asn	Thr	Gln	His	Pro	Glu	
		195					200					205				
GAC	AGC	GAC	GAG	AGT	CTG	TCG	GAC	GAC	GAT	TCC	CAG	CAC	CAC	CGC	AGC	672
Asp	Ser	Asp	Glu	Ser	Leu	Ser	Asp	Asp	Asp	Ser	Gln	His	His	Arg	Ser	
	210					215					220					
GAG	CTG	ACG	CGA	CGG	CCG	TCG	TAC	AAT	AAG	ATC	TTC	ACC	GAG	ATC	AGC	720
Glu	Leu	Thr	Arg	Arg	Pro	Ser	Tyr	Asn	Lys	Ile	Phe	Thr	Glu	Ile	Ser	
225					230					235					240	
GGT	CCG	GAC	ATG	AGC	GGC	GCA	TCG	CTT	CCC	ATG	TCC	GAC	GGC	GTG	CTC	768
Gly	Pro	Asp	Met	Ser	Gly	Ala	Ser	Leu	Pro	Met	Ser	Asp	Gly	Val	Leu	
				245					250					255		
AAT	TCC	CAG	CTG	GTG	GGG	ACC	GGA	GCG	GGG	GGC	AAT	GCG	GCG	AAC	AGC	816
Asn	Ser	Gln	Leu	Val	Gly	Thr	Gly	Ala	Gly	Gly	Asn	Ala	Ala	Asn	Ser	
			260				265						270			
TCC	CTG	ATG	CAA	TTG	GAT	CCC	ACG	TAC	TAC	CTG	TCC	AAT	CGG	ATG	TCC	864
Ser	Leu	Met	Gln	Leu	Asp	Pro	Thr	Tyr	Tyr	Leu	Ser	Asn	Arg	Met	Ser	
		275				280						285				
TAC	AAC	ACC	AAC	AAC	AGC	GGG	ATA	GCG	GAG	GAT	CAG	ACC	CGT	AAG	CGC	912
Tyr	Asn	Thr	Asn	Asn	Ser	Gly	Ile	Ala	Glu	Asp	Gln	Thr	Arg	Lys	Arg	
	290					295					300					
GAG	ATC	CGG	CTG	CAG	AAG	AAC	AGG	GAG	GCG	GCG	CGT	GAG	TGC	CGG	CGC	960
Glu	Ile	Arg	Leu	Gln	Lys	Asn	Arg	Glu	Ala	Ala	Arg	Glu	Cys	Arg	Arg	
305					310					315					320	
AAG	AAG	AAG	GAG	TAC	ATC	AAG	TGC	CTG	GAG	AAT	CGA	GTG	GCG	GTG	CTA	1008
Lys	Lys	Lys	Glu	Tyr	Ile	Lys	Cys	Leu	Glu	Asn	Arg	Val	Ala	Val	Leu	
				325					330					335		
GAG	AAC	CAA	AAC	AAA	GCG	CTC	ATC	GAG	GAG	CTG	AAG	TCG	CTC	AAG	GAG	1056
Glu	Asn	Gln	Asn	Lys	Ala	Leu	Ile	Glu	Glu	Leu	Lys	Ser	Leu	Lys	Glu	
			340					345					350			

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CTC TAT TGT CAG ACC AAG AAC GAT TGA
 Leu Tyr Cys Gln Thr Lys Asn Asp
 355 360

1083

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Asn Ser Ile Val Glu Glu Asn Gly Asn Ser Ser Ala Ala Ser
 1 5 10 15
 Gly Ser Asn Asp Val Val Asp Val Val Ala Gln Gln Ala Ala Ala Ala
 20 25 30
 Val Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn
 35 40 45
 Pro Gln Gln Gln Gln Gln Asn Pro Gln Ser Thr Thr Ala Gly Gly Pro
 50 55 60
 Thr Gly Ala Thr Asn Asn Ala Gln Gly Gly Gly Val Ser Ser Val Leu
 65 70 75 80
 Thr Thr Thr Ala Asn Cys Asn Ile Gln Tyr Pro Ile Gln Thr Leu Ala
 85 90 95
 Gln His Gly Leu Gln Val Ser Ile Trp Gly Pro Gly Ala Trp Cys Gln
 100 105 110
 Leu Ser Ser Val Arg Cys Tyr Gly Ser Gln Pro Glu Val Ala Thr Lys
 115 120 125
 Asp Val Gln Ser Val Ile Gln Ala Asn Pro Ser Gly Val Ile Gln Thr
 130 135 140
 Ala Ala Gly Thr Gln Gln Gln Gln Gln Ala Leu Ala Ala Ala Thr Ala
 145 150 155 160
 Met Gln Lys Val Val Tyr Val Ala Lys Pro Pro Asn Ser Thr Val Ile
 165 170 175
 His Thr Thr Pro Gly Asn Ala Val Gln Val Arg Asn Lys Ile Pro Pro
 180 185 190
 Thr Phe Pro Cys Lys Ile Lys Pro Glu Pro Asn Thr Gln His Pro Glu
 195 200 205
 Asp Ser Asp Glu Ser Leu Ser Asp Asp Asp Ser Gln His His Arg Ser
 210 215 220
 Glu Leu Thr Arg Arg Pro Ser Tyr Asn Lys Ile Phe Thr Glu Ile Ser
 225 230 235 240

Gly	Pro	Asp	Met	Ser 245	Gly	Ala	Ser	Leu	Pro 250	Met	Ser	Asp	Gly	Val 255	Leu
Asn	Ser	Gln	Leu 260	Val	Gly	Thr	Gly	Ala 265	Gly	Gly	Asn	Ala	Ala 270	Asn	Ser
Ser	Leu	Met 275	Gln	Leu	Asp	Pro	Thr 280	Tyr	Tyr	Leu	Ser	Asn 285	Arg	Met	Ser
Tyr	Asn 290	Thr	Asn	Asn	Ser	Gly 295	Ile	Ala	Glu	Asp	Gln 300	Thr	Arg	Lys	Arg
Glu 305	Ile	Arg	Leu	Gln	Lys 310	Asn	Arg	Glu	Ala 315	Ala	Arg	Glu	Cys	Arg	Arg 320
Lys	Lys	Lys	Glu	Tyr 325	Ile	Lys	Cys	Leu	Glu 330	Asn	Arg	Val	Ala	Val 335	Leu
Glu	Asn	Gln	Asn 340	Lys	Ala	Leu	Ile	Glu 345	Glu	Leu	Lys	Ser	Leu 350	Lys	Glu
Leu	Tyr	Cys 355	Gln	Thr	Lys	Asn	Asp 360								

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Lys Arg Glu Ile Arg Leu Gln Lys Asn Arg Glu Ala Ala Arg Glu
1 5 10 15

Cys Arg Arg Lys Lys Lys Glu Tyr Ile Lys Cys Leu Glu Asn Arg Val
20 25 30

Ala Val Leu Glu Asn Gln Asn Lys Ala Leu Ile Glu Glu Leu Lys Ser
35 40 45

Leu Lys Glu Leu Tyr Cys
50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Arg Lys Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu
1           5           10           15
Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val
20           25           30
Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala
35           40           45
Leu Lys Asp Leu Tyr Cys
50

```

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Arg Lys Arg Glu Leu Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu
1           5           10           15
Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val
20           25           30
Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala
35           40           45
Leu Lys Asp Leu Tyr Cys
50

```

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Leu Lys Arg Glu Ile Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu
1           5           10           15
Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val
20           25           30
Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Thr
35           40           45

```

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Leu Lys Asp Leu Tyr Ser
50

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG TTA CTC GGA GAA AAT ATG TTT TCT ACT TTC ACA TCG TTA GAT GCT	48
Met Leu Leu Gly Glu Asn Met Phe Ser Thr Phe Thr Ser Leu Asp Ala	
1 5 10 15	
GCT ACC GCT ACA ACC AAC ACC GGT GAA TTC TTA ATG AAT GAA TCT CCA	96
Ala Thr Ala Thr Asn Thr Gly Glu Phe Leu Met Asn Glu Ser Pro	
20 25 30	
AGG CAA GAA GCC GGT GAC TTA ATG TTG GAT AGT CTG GAT TTC AAC ATT	144
Arg Gln Glu Ala Gly Asp Leu Met Leu Asp Ser Leu Asp Phe Asn Ile	
35 40 45	
ATG GGC GAA AAC CTG GCA GAT GAT TTC CAG ACC TCG GCT TCA CCA GCT	192
Met Gly Glu Asn Leu Ala Asp Asp Phe Gln Thr Ser Ala Ser Pro Ala	
50 55 60	
TCG GAG GAC AAG ATG ACT CCT TTC GTT GTT GAT ACC AAT GTT TTT GAA	240
Ser Glu Asp Lys Met Thr Pro Phe Val Val Asp Thr Asn Val Phe Glu	
65 70 75 80	
TCC GTC TTC AAG AAC ACC GAA GAT ACC CTT CTA GGA GAT ATC GAC AAT	288
Ser Val Phe Lys Asn Thr Glu Asp Thr Leu Leu Gly Asp Ile Asp Asn	
85 90 95	
GTT GGT ATT GTT GAC ACG GAG TTG AAG GAG ATG TTC GAT TTG GTT GAC	336
Val Gly Ile Val Asp Thr Glu Leu Lys Glu Met Phe Asp Leu Val Asp	
100 105 110	
TCG GAA ATC AAT AAC GGC ACT CCT ATC AAG CAG GAA GAA AAG GAT GAT	384
Ser Glu Ile Asn Asn Gly Thr Pro Ile Lys Gln Glu Glu Lys Asp Asp	
115 120 125	
TTG GAA TTT ACT TCA AGA TCC CAG TCC ACC TCA GCT CTC TTG TCG TCG	432
Leu Glu Phe Thr Ser Arg Ser Gln Ser Thr Ser Ala Leu Leu Ser Ser	
130 135 140	
AAA TCG ACT TCT GCT TCT CCA GCT GAT GCT GCC GCT GCA TGT GCA AGT	480
Lys Ser Thr Ser Ala Ser Pro Ala Asp Ala Ala Ala Ala Cys Ala Ser	
145 150 155 160	

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CCT TCG TCA TCG TCT TGT AAA AGA TCC TAT TCT TCT GCT CAG CTA GAA	528
Pro Ser Ser Ser Ser Cys Lys Arg Ser Tyr Ser Ser Ala Gln Leu Glu	
165 170 175	
ACT ACG GGT TCG GAT GCT CCA AAG AAA GAT AAG CTG GGC TGC ACC CCT	576
Thr Thr Gly Ser Asp Ala Pro Lys Lys Asp Lys Leu Gly Cys Thr Pro	
180 185 190	
TAC ACT AGA AAA CAG AGA AAC AAT CCA TTA CCT CCG GTC ATT CCA AAG	624
Tyr Thr Arg Lys Gln Arg Asn Asn Pro Leu Pro Pro Val Ile Pro Lys	
195 200 205	
GGT CAG GAT GTT GCT TCT ATG AAA AGG GCA AGA AAC ACT GAG GCC GCA	672
Gly Gln Asp Val Ala Ser Met Lys Arg Ala Arg Asn Thr Glu Ala Ala	
210 215 220	
AGA AGA TCA AGA GCC AGA AAA ATG GAA AGA ATG TCC CAA CTT GAA GAA	720
Arg Arg Ser Arg Ala Arg Lys Met Glu Arg Met Ser Gln Leu Glu Glu	
225 230 235 240	
AAG TGT CAA AGC TTG TTG AAG GAA AAC GAC GAC TTG AAA GCT CAA GTT	768
Lys Cys Gln Ser Leu Leu Lys Glu Asn Asp Asp Leu Lys Ala Gln Val	
245 250 255	
CAA GCT TTG AAG AAA TTA CTT GGA CAA CAA	798
Gln Ala Leu Lys Lys Leu Leu Gly Gln Gln	
260 265	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Leu Leu Gly Glu Asn Met Phe Ser Thr Phe Thr Ser Leu Asp Ala	
1 5 10 15	
Ala Thr Ala Thr Thr Asn Thr Gly Glu Phe Leu Met Asn Glu Ser Pro	
20 25 30	
Arg Gln Glu Ala Gly Asp Leu Met Leu Asp Ser Leu Asp Phe Asn Ile	
35 40 45	
Met Gly Glu Asn Leu Ala Asp Asp Phe Gln Thr Ser Ala Ser Pro Ala	
50 55 60	
Ser Glu Asp Lys Met Thr Pro Phe Val Val Asp Thr Asn Val Phe Glu	
65 70 75 80	
Ser Val Phe Lys Asn Thr Glu Asp Thr Leu Leu Gly Asp Ile Asp Asn	
85 90 95	
Val Gly Ile Val Asp Thr Glu Leu Lys Glu Met Phe Asp Leu Val Asp	
100 105 110	

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Ser Glu Ile Asn Asn Gly Thr Pro Ile Lys Gln Glu Glu Lys Asp Asp
 115 120 125
 Leu Glu Phe Thr Ser Arg Ser Gln Ser Thr Ser Ala Leu Leu Ser Ser
 130 135 140
 Lys Ser Thr Ser Ala Ser Pro Ala Asp Ala Ala Ala Cys Ala Ser
 145 150 155 160
 Pro Ser Ser Ser Ser Cys Lys Arg Ser Tyr Ser Ser Ala Gln Leu Glu
 165 170 175
 Thr Thr Gly Ser Asp Ala Pro Lys Lys Asp Lys Leu Gly Cys Thr Pro
 180 185 190
 Tyr Thr Arg Lys Gln Arg Asn Asn Pro Leu Pro Pro Val Ile Pro Lys
 195 200 205
 Gly Gln Asp Val Ala Ser Met Lys Arg Ala Arg Asn Thr Glu Ala Ala
 210 215 220
 Arg Arg Ser Arg Ala Arg Lys Met Glu Arg Met Ser Gln Leu Glu Glu
 225 230 235 240
 Lys Cys Gln Ser Leu Leu Lys Glu Asn Asp Asp Leu Lys Ala Gln Val
 245 250 255
 Gln Ala Leu Lys Lys Leu Leu Gly Gln Gln
 260 265

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ser Gln His Phe Thr Ser Ile Phe Glu Asn Leu Arg Phe Val Thr
 1 5 10 15
 Ile Lys Arg Ala Thr Asn Ala Gln Gln Gln Gln Gln Gln Gln Gln
 20 25 30
 Gln Gln Leu Gln Gln Gln Gln Gln Gln Leu Gln Gln Gln Lys Ala Gln
 35 40 45
 Thr Gln Gln Gln Asn Ser Arg Lys Ile Lys Thr Gln Ala Thr Pro Thr
 50 55 60
 Leu Asn Gly Asn Gly Leu Leu Ser Gly Asn Pro Asn Gly Gly Gly Gly
 65 70 75 80
 Asp Ser Ser Pro Ser His Glu Val Asp His Pro Gly Gly Ala Gln Gly
 85 90 95

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Ala Gln Ala Ala Gly Gly Leu Pro Ser Leu Ser Gly Thr Pro Leu Arg
 100 105 110
 His His Lys Arg Ala Ser Ile Ser Thr Ala Ser Pro Pro Ile Arg Glu
 115 120 125
 Arg Arg Gly Thr Asn Thr Ser Ile Val Val Glu Leu Asp Gly Ser Gly
 130 135 140
 Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Gly Val Gly Gln Gly Ala
 145 150 155 160
 Gly Cys Pro Pro Ser Gly Ser Cys Thr Ala Ser Gly Lys Ser Ser Arg
 165 170 175
 Glu Leu Ser Pro Ser Pro Lys Asn Gln Gln Gln Pro Arg Lys Met Ser
 180 185 190
 Gln Asp Tyr Arg Ser Arg Ala Gly Ser Phe Met His Leu Asp Asp Glu
 195 200 205
 Gly Arg Ser Leu Leu Met Arg Lys Pro Met Arg Leu Lys Asn Ile Glu
 210 215 220
 Gly Arg Pro Glu Val Tyr Asp Thr Leu His Cys Lys Gly Arg Glu Ile
 225 230 235 240
 Leu Ser Cys Ser Lys Ala Thr Cys Thr Ser Ser Ile Met Asn Ile Gly
 245 250 255
 Asn Ala Ala Val Glu Ala Arg Lys Ser Asp Leu Ile Leu Glu His Ala
 260 265 270
 Lys Asp Phe Leu Glu Gln Tyr Phe Thr Ser Ile Lys Arg Thr Ser Cys
 275 280 285
 Thr Ala His Glu Thr Arg Trp Lys Gln Val Arg Gln Ser Ile Glu Thr
 290 295 300
 Thr Gly His Tyr Gln Leu Thr Glu Thr Glu Leu Ile Tyr Gly Ala Lys
 305 310 315 320
 Leu Ala Trp Arg Asn Ser Ser Arg Cys Ile Gly Arg Ile Gln Trp Ser
 325 330 335
 Lys Leu Gln Val Phe Asp Cys Arg Tyr Val Thr Thr Thr Ser Gly Met
 340 345 350
 Phe Glu Ala Ile Cys Asn His Ile Lys Tyr Ala Thr Asn Lys Gly Asn
 355 360 365
 Leu Arg Ser Ala Ile Thr Ile Phe Pro Gln Arg Thr Asp Ala Lys His
 370 375 380
 Asp Tyr Arg Ile Trp Asn Asn Gln Leu Ile Ser Tyr Ala Gly Tyr Lys
 385 390 395 400
 Gln Ala Asp Gly Lys Ile Ile Gly Asp Pro Met Asn Val Glu Phe Thr
 405 410 415
 Glu Val Cys Thr Lys Leu Gly Trp Lys Ser Lys Gly Ser Glu Trp Asp
 420 425 430

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Ile Leu Pro Leu Val Val Ser Ala Asn Gly His Asp Pro Asp Tyr Phe
 435 440 445
 Asp Tyr Pro Pro Glu Leu Ile Leu Glu Val Pro Leu Thr His Pro Lys
 450 455 460
 Phe Glu Trp Phe Ser Asp Leu Gly Leu Arg Trp Tyr Ala Leu Pro Ala
 465 470 475 480
 Val Ser Ser Met Leu Phe Asp Val Gly Gly Ile Gln Phe Thr Ala Thr
 485 490 495
 Thr Phe Ser Gly Trp Tyr Met Ser Thr Glu Ile Gly Ser Arg Asn Leu
 500 505 510
 Cys Asp Thr Asn Arg Arg Asn Met Leu Glu Thr Val Ala Leu Lys Met
 515 520 525
 Gln Leu Asp Thr Arg Thr Pro Thr Ser Leu Trp Lys Asp Lys Ala Val
 530 535 540
 Val Glu Met Asn Ile Ala Val Leu His Ser Tyr Gln Ser Arg Asn Val
 545 550 555 560
 Thr Ile Val Asp His His Thr Ala Ser Glu Ser Phe Met Lys His Phe
 565 570 575
 Glu Asn Glu Ser Lys Leu Arg Asn Gly Cys Pro Ala Asp Trp Ile Trp
 580 585 590
 Ile Val Pro Pro Leu Ser Gly Ser Ile Thr Pro Val Phe His Gln Glu
 595 600 605
 Met Ala Leu Tyr Tyr Leu Lys Pro Ser Phe Glu Tyr Gln Asp Pro Ala
 610 615 620
 Trp Arg Thr His Val Trp Lys Lys Gly Arg Gly Glu Ser Lys Gly Lys
 625 630 635 640
 Lys Pro Arg Arg Lys Phe Asn Phe Lys Gln Ile Ala Arg Ala Val Lys
 645 650 655
 Phe Thr Ser Lys Leu Phe Gly Arg Ala Leu Ser Lys Arg Ile Lys Ala
 660 665 670
 Thr Val Leu Tyr Ala Thr Glu Thr Gly Lys Ser Glu Gln Tyr Ala Lys
 675 680 685
 Gln Leu Cys Glu Leu Leu Gly His Ala Phe Asn Ala Gln Ile Tyr Cys
 690 695 700
 Met Ser Asp Tyr Asp Ile Ser Ser Ile Glu His Glu Ala Leu Leu Ile
 705 710 715 720
 Val Val Ala Ser Thr Phe Gly Asn Gly Asp Pro Pro Glu Asn Gly Glu
 725 730 735
 Leu Phe Ser Gln Glu Leu Tyr Ala Met Arg Val Gln Glu Ser Ser Glu
 740 745 750
 His Gly Leu Gln Asp Ser Ser Ile Gly Ser Ser Lys Ser Phe Met Lys
 755 760 765

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Ala Ser Ser Arg Gln Glu Phe Met Lys Leu Pro Leu Gln Gln Val Lys
 770 775 780
 Arg Ile Asp Arg Trp Asp Ser Leu Arg Gly Ser Thr Ser Asp Thr Phe
 785 790 795 800
 Thr Glu Glu Thr Phe Gly Pro Leu Ser Asn Val Arg Phe Ala Val Phe
 805 810 815
 Ala Leu Gly Ser Ser Ala Tyr Pro Asn Phe Cys Ala Phe Gly Gln Tyr
 820 825 830
 Val Asp Asn Ile Leu Gly Glu Leu Gly Gly Glu Arg Leu Leu Arg Val
 835 840 845
 Ala Tyr Gly Asp Glu Met Cys Gly Gln Glu Gln Ser Phe Arg Lys Trp
 850 855 860
 Ala Pro Glu Val Phe Lys Leu Ala Cys Glu Thr Phe Cys Leu Asp Pro
 865 870 875 880
 Glu Glu Ser Leu Ser Asp Ala Ser Leu Ala Leu Gln Asn Asp Ser Leu
 885 890 895
 Thr Val Asn Thr Val Arg Leu Val Pro Ser Ala Asn Lys Gly Ser Leu
 900 905 910
 Asp Ser Ser Leu Ser Lys Tyr His Asn Lys Lys Val His Cys Cys Lys
 915 920 925
 Ala Lys Ala Lys Pro His Asn Leu Thr Arg Leu Ser Glu Gly Ala Lys
 930 935 940
 Thr Thr Met Leu Leu Glu Ile Cys Ala Pro Gly Leu Glu Tyr Glu Pro
 945 950 955 960
 Gly Asp His Val Gly Ile Phe Pro Ala Asn Arg Thr Glu Leu Val Asp
 965 970 975
 Gly Leu Leu Asn Arg Leu Val Gly Val Asp Asn Pro Asp Glu Val Leu
 980 985 990
 Gln Leu Gln Leu Leu Lys Glu Lys Gln Thr Ser Asn Gly Ile Phe Lys
 995 1000 1005
 Cys Trp Glu Pro His Asp Lys Ile Pro Pro Asp Thr Leu Arg Asn Leu
 1010 1015 1020
 Leu Ala Arg Phe Phe Asp Leu Thr Thr Pro Pro Ser Arg Gln Leu Leu
 1025 1030 1035 1040
 Thr Leu Leu Ala Gly Phe Cys Glu Asp Thr Ala Asp Lys Glu Arg Leu
 1045 1050 1055
 Glu Leu Leu Val Asn Asp Ser Ser Ala Tyr Glu Asp Trp Arg His Trp
 1060 1065 1070
 Arg Leu Pro His Leu Leu Asp Val Leu Glu Glu Phe Pro Ser Cys Arg
 1075 1080 1085
 Pro Pro Ala Pro Leu Leu Leu Ala Gln Leu Thr Pro Leu Gln Pro Arg
 1090 1095 1100

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Phe Tyr Ser Ile Ser Ser Ser Pro Arg Arg Val Ser Asp Glu Ile His
 1105 1110 1115 1120
 Leu Thr Val Ala Ile Val Lys Tyr Arg Cys Glu Asp Gly Gln Gly Asp
 1125 1130 1135
 Glu Arg Tyr Gly Val Cys Ser Asn Tyr Leu Ser Gly Leu Arg Ala Asp
 1140 1145 1150
 Asp Glu Leu Phe Met Phe Val Arg Ser Ala Leu Gly Phe His Leu Pro
 1155 1160 1165
 Ser Asp Arg Ser Arg Pro Ile Ile Leu Ile Gly Pro Gly Thr Gly Ile
 1170 1175 1180
 Ala Pro Phe Arg Ser Phe Trp Gln Glu Phe Gln Val Leu Arg Asp Leu
 1185 1190 1195 1200
 Asp Pro Thr Ala Lys Leu Pro Lys Met Trp Leu Phe Phe Gly Cys Arg
 1205 1210 1215
 Asn Arg Asp Val Asp Leu Tyr Ala Glu Glu Lys Ala Glu Leu Gln Lys
 1220 1225 1230
 Asp Gln Ile Leu Asp Arg Val Phe Leu Ala Leu Ser Arg Glu Gln Ala
 1235 1240 1245
 Ile Pro Lys Thr Tyr Val Gln Asp Leu Ile Glu Gln Glu Phe Asp Ser
 1250 1255 1260
 Leu Tyr Gln Leu Ile Val Gln Glu Arg Gly His Ile Tyr Val Cys Gly
 1265 1270 1275 1280
 Asp Val Thr Met Ala Glu His Val Tyr Gln Thr Ile Arg Lys Cys Ile
 1285 1290 1295
 Ala Gly Lys Glu Gln Lys Ser Glu Ala Glu Val Glu Thr Phe Leu Leu
 1300 1305 1310
 Thr Leu Arg Asp Glu Ser Arg Tyr His Glu Asp Ile Phe Gly Ile Thr
 1315 1320 1325
 Leu Arg Thr Ala Glu Ile His Thr Lys Ser Arg Ala Thr Ala Arg Ile
 1330 1335 1340
 Arg Met Ala Ser Gln Pro
 1345 1350

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Asn Leu Lys Ser Val Gly Gln Glu Pro Gly Pro Pro Cys Gly
 1 5 10 15
 Leu Gly Leu Gly Leu Gly Leu Gly Leu Cys Gly Lys Gln Gly Pro Ala
 20 25 30
 Ser Pro Ala Pro Glu Pro Ser Arg Ala Pro Ala Pro Ala Thr Pro His
 35 40 45
 Ala Pro Asp His Ser Pro Ala Pro Asn Ser Pro Thr Leu Thr Arg Pro
 50 55 60
 Pro Glu Gly Pro Lys Phe Pro Arg Val Lys Asn Trp Glu Leu Gly Ser
 65 70 75 80
 Ile Thr Tyr Asp Thr Leu Cys Ala Gln Ser Gln Gln Asp Gly Pro Cys
 85 90 95
 Thr Pro Arg Arg Cys Leu Gly Ser Leu Val Leu Pro Arg Lys Leu Gln
 100 105 110
 Thr Arg Pro Ser Pro Gly Pro Pro Pro Ala Glu Gln Leu Leu Ser Gln
 115 120 125
 Ala Arg Asp Phe Ile Asn Gln Tyr Tyr Ser Ser Ile Lys Arg Ser Gly
 130 135 140
 Ser Gln Ala His Glu Glu Arg Leu Gln Glu Val Glu Ala Glu Val Ala
 145 150 155 160
 Ser Thr Gly Thr Ile His Leu Arg Glu Ser Glu Leu Val Phe Gly Ala
 165 170 175
 Lys Gln Ala Trp Arg Asn Ala Pro Arg Cys Val Gly Arg Ile Gln Trp
 180 185 190
 Gly Lys Leu Gln Val Phe Asp Ala Arg Asp Cys Ser Ser Ala Gln Glu
 195 200 205
 Met Phe Thr Tyr Ile Cys Asn His Ile Lys Tyr Ala Thr Asn Arg Gly
 210 215 220
 Asn Leu Arg Ser Ala Ile Thr Val Phe Pro Gln Arg Ala Pro Gly Arg
 225 230 235 240
 Gly Asp Phe Arg Ile Trp Asn Ser Gln Leu Val Arg Tyr Ala Gly Tyr
 245 250 255
 Arg Gln Gln Asp Gly Ser Val Arg Gly Asp Pro Ala Asn Val Glu Ile
 260 265 270
 Thr Glu Leu Cys Ile Gln His Gly Trp Thr Pro Gly Asn Gly Arg Phe
 275 280 285
 Asp Val Leu Pro Leu Leu Leu Gln Ala Pro Asp Glu Ala Pro Glu Leu
 290 295 300
 Phe Val Leu Pro Pro Glu Leu Val Leu Glu Val Pro Leu Gly Ala Pro
 305 310 315 320

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His Thr Gly Val Val Arg Gly Pro Gly Leu Arg Trp Tyr Ala Leu Pro
 325 330 335
 Ala Val Ser Asn Met Leu Leu Glu Ile Gly Gly Leu Glu Phe Ser Ala
 340 345 350
 Ala Pro Phe Ser Gly Trp Tyr Met Ser Thr Glu Ile Gly Thr Arg Asn
 355 360 365
 Leu Cys Asp Pro His Arg Tyr Asn Ile Leu Glu Asp Val Ala Val Cys
 370 375 380
 Met Asp Leu Asp Thr Arg Thr Thr Ser Ser Leu Trp Lys Asp Lys Ala
 385 390 395 400
 Ala Val Glu Ile Asn Leu Ala Val Leu His Ser Phe Gln Leu Ala Lys
 405 410 415
 Val Thr Ile Val Asp His His Ala Ala Thr Val Ser Phe Met Lys His
 420 425 430
 Leu Asp Asn Glu Gln Lys Ala Arg Gly Gly Cys Pro Ala Asp Trp Ala
 435 440 445
 Trp Ile Val Pro Pro Ile Tyr Gly Ser Leu Pro Pro Val Phe His Gln
 450 455 460
 Glu Met Val Asn Tyr Ile Leu Ser Pro Ala Phe Arg Tyr Gln Pro Asp
 465 470 475 480
 Pro Trp Lys Gly Ser Ala Thr Lys Gly Ala Gly Ile Thr Arg Lys Lys
 485 490 495
 Thr Phe Lys Glu Val Ala Asn Ala Val Lys Ile Ser Ala Ser Leu Met
 500 505 510
 Gly Thr Leu Met Ala Lys Arg Val Lys Ala Thr Ile Leu Tyr Ala Ser
 515 520 525
 Glu Thr Gly Arg Ala Gln Ser Tyr Ala Gln Gln Leu Gly Arg Leu Phe
 530 535 540
 Arg Lys Ala Phe Asp Pro Arg Val Leu Cys Met Asp Glu Tyr Asp Val
 545 550 555 560
 Val Ser Leu Glu His Glu Ala Leu Val Leu Val Val Thr Ser Thr Phe
 565 570 575
 Gly Asn Gly Asp Pro Pro Glu Asn Gly Glu Ser Phe Ala Ala Ala Leu
 580 585 590
 Met Glu Met Ser Gly Pro Tyr Asn Ser Ser Pro Arg Pro Glu Gln His
 595 600 605
 Lys Ser Tyr Lys Ile Arg Phe Asn Ser Val Ser Cys Ser Asp Pro Leu
 610 615 620
 Val Ser Ser Trp Arg Arg Lys Arg Lys Glu Ser Ser Asn Thr Asp Ser
 625 630 635 640
 Ala Gly Ala Leu Gly Thr Leu Arg Phe Cys Val Phe Gly Leu Gly Ser
 645 650 655

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Arg Ala Tyr Pro His Phe Cys Ala Phe Ala Arg Ala Val Asp Thr Arg
 660 665 670
 Leu Glu Glu Leu Gly Gly Glu Arg Leu Leu Gln Leu Gly Gln Gly Asp
 675 680 685
 Glu Leu Cys Gly Gln Glu Glu Ala Phe Arg Gly Trp Ala Lys Ala Ala
 690 695 700
 Phe Gln Ala Ser Cys Glu Thr Phe Cys Val Gly Glu Glu Ala Lys Ala
 705 710 715 720
 Ala Ala Gln Asp Ile Phe Ser Pro Lys Arg Ser Trp Lys Arg Gln Arg
 725 730 735
 Tyr Arg Leu Ser Ala Gln Ala Glu Gly Leu Gln Leu Leu Pro Gly Leu
 740 745 750
 Ile His Val His Arg Arg Lys Met Phe Gln Ala Thr Val Leu Ser Val
 755 760 765
 Glu Asn Leu Gln Ser Ser Lys Ser Thr Arg Ala Thr Ile Leu Val Arg
 770 775 780
 Leu Asp Thr Ala Gly Gln Glu Gly Leu Gln Tyr Gln Pro Gly Asp His
 785 790 795 800
 Ile Gly Ile Ser Ala Pro Asn Arg Pro Gly Leu Val Glu Ala Leu Leu
 805 810 815
 Ser Arg Val Glu Asp Pro Pro Pro Pro Thr Glu Ser Val Ala Val Glu
 820 825 830
 Gln Leu Glu Lys Gly Ser Pro Gly Gly Pro Pro Pro Ser Trp Val Arg
 835 840 845
 Asp Pro Arg Leu Pro Pro Cys Thr Val Arg Gln Ala Leu Thr Phe Phe
 850 855 860
 Leu Asp Ile Thr Ser Pro Pro Ser Pro Arg Leu Leu Arg Leu Leu Ser
 865 870 875 880
 Thr Leu Ala Glu Glu Pro Ser Glu Gln Gln Glu Leu Glu Thr Leu Ser
 885 890 895
 Gln Asp Pro Arg Arg Tyr Glu Glu Trp Lys Leu Val Arg Cys Pro Thr
 900 905 910
 Leu Leu Glu Val Leu Glu Gln Phe Pro Ser Val Ala Leu Pro Ala Pro
 915 920 925
 Leu Leu Leu Thr Gln Leu Pro Leu Leu Gln Pro Arg Tyr Tyr Ser Val
 930 935 940
 Ser Ser Ala Pro Asn Ala His Pro Gly Glu Val His Leu Thr Val Ala
 945 950 955 960
 Val Leu Ala Tyr Arg Thr Gln Asp Gly Leu Gly Pro Leu His Tyr Gly
 965 970 975
 Val Cys Ser Thr Trp Leu Ser Gln Leu Lys Thr Gly Asp Pro Val Pro
 980 985 990

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Cys Phe Ile Arg Gly Ala Pro Ser Phe Arg Leu Pro Pro Asp Pro Tyr
 995 1000 1005
 Val Pro Cys Ile Leu Val Gly Pro Gly Thr Gly Ile Ala Pro Phe Arg
 1010 1015 1020
 Gly Phe Trp Gln Glu Arg Leu His Asp Ile Glu Ser Lys Gly Leu Gln
 1025 1030 1035 1040
 Pro His Pro Met Thr Leu Val Phe Gly Cys Arg Cys Ser Gln Leu Asp
 1045 1050 1055
 His Leu Tyr Arg Asp Glu Val Gln Asp Ala Gln Glu Arg Gly Val Phe
 1060 1065 1070
 Gly Arg Val Leu Thr Ala Phe Ser Arg Glu Pro Asp Ser Pro Lys Thr
 1075 1080 1085
 Tyr Val Gln Asp Ile Leu Arg Thr Glu Leu Ala Ala Glu Val His Arg
 1090 1095 1100
 Val Leu Cys Leu Glu Arg Gly His Met Phe Val Cys Gly Asp Val Thr
 1105 1110 1115 1120
 Met Ala Thr Ser Val Leu Gln Thr Val Gln Arg Ile Leu Ala Thr Glu
 1125 1130 1135
 Gly Asp Met Glu Leu Asp Glu Ala Gly Asp Val Ile Gly Val Leu Arg
 1140 1145 1150
 Asp Gln Gln Arg Tyr His Glu Asp Ile Phe Gly Leu Thr Leu Arg Thr
 1155 1160 1165
 Gln Glu Val Thr Ser Arg Ile Arg Thr Gln Ser Phe Ser Leu Gln Glu
 1170 1175 1180
 Arg His Leu Arg Gly Ala Val Pro Trp Ala Phe Asp Pro Pro Gly Pro
 1185 1190 1195 1200
 Asp Thr Pro Gly Pro
 1205

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Glu Asn Thr Phe Gly Val Gln Gln Ile Gln Pro Asn Val Ile
 1 5 10 15
 Ser Val Arg Leu Phe Lys Arg Lys Val Gly Gly Leu Gly Phe Leu Val
 20 25 30

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Lys Glu Arg Val Ser Lys Pro Pro Val Ile Ile Ser Asp Leu Ile Arg
 35 40 45
 Gly Gly Ala Ala Glu Gln Ser Gly Leu Ile Gln Ala Gly Asp Ile Ile
 50 55 60
 Leu Ala Val Asn Asp Arg Pro Leu Val Asp Leu Ser Tyr Asp Ser Ala
 65 70 75 80
 Leu Glu Val Leu Arg Gly Ile Ala Ser Glu Thr His Val Val Leu Ile
 85 90 95
 Leu Arg Gly Pro Glu Gly Phe Thr Thr His Leu Glu Thr Thr Phe Thr
 100 105 110
 Gly Asp Gly Thr Pro Lys Thr Ile Arg Val Thr Gln Pro Leu Gly Pro
 115 120 125
 Pro Thr Lys Ala Val Asp Leu Ser His Gln Pro Ser Ala Ser Lys Asp
 130 135 140
 Gln Ser Leu Ala Val Asp Arg Val Thr Gly Leu Gly Asn Gly Pro Gln
 145 150 155 160
 His Ala Gln Gly His Gly Gln Gly Ala Gly Ser Val Ser Gln Ala Asn
 165 170 175
 Gly Val Ala Ile Asp Pro Thr Met Lys Ser Thr Lys Ala Asn Leu Gln
 180 185 190
 Asp Ile Gly Glu His Asp Glu Leu Leu Lys Glu Ile Glu Pro Val Leu
 195 200 205
 Ser Ile Leu Asn Ser Gly Ser Lys Ala Thr Asn Arg Gly Gly Pro Ala
 210 215 220
 Lys Ala Glu Met Lys Asp Thr Gly Ile Gln Val Asp Arg Asp Leu Asp
 225 230 235 240
 Gly Lys Ser His Lys Ala Pro Pro Leu Gly Gly Asp Asn Asp Arg Val
 245 250 255
 Phe Asn Asp Leu Trp Gly Lys Asp Asn Val Pro Val Ile Leu Asn Asn
 260 265 270
 Pro Tyr Ser Glu Lys Glu Gln Ser Pro Thr Ser Gly Lys Gln Ser Pro
 275 280 285
 Thr Lys Asn Gly Ser Pro Ser Arg Cys Pro Arg Phe Leu Lys Val Lys
 290 295 300
 Asn Trp Glu Thr Asp Val Val Leu Thr Asp Thr Leu His Leu Lys Ser
 305 310 315 320
 Thr Leu Glu Thr Gly Cys Thr Glu His Ile Cys Met Gly Ser Ile Met
 325 330 335
 Leu Pro Ser Gln His Thr Arg Lys Pro Glu Asp Val Arg Thr Lys Asp
 340 345 350
 Gln Leu Phe Pro Leu Ala Lys Glu Phe Leu Asp Gln Tyr Tyr Ser Ser
 355 360 365

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Ile Lys Arg Phe Gly Ser Lys Ala His Met Asp Arg Leu Glu Glu Val
 370 375 380
 Asn Lys Glu Ile Glu Ser Thr Ser Thr Tyr Gln Leu Lys Asp Thr Glu
 385 390 395 400
 Leu Ile Tyr Gly Ala Lys His Ala Trp Arg Asn Ala Ser Arg Cys Val
 405 410 415
 Gly Arg Ile Gln Trp Ser Lys Leu Gln Val Phe Asp Ala Arg Asp Cys
 420 425 430
 Thr Thr Ala His Gly Met Phe Asn Tyr Ile Cys Asn His Val Lys Tyr
 435 440 445
 Ala Thr Asn Lys Gly Asn Leu Arg Ser Ala Ile Thr Ile Phe Pro Gln
 450 455 460
 Arg Thr Asp Gly Lys His Asp Phe Arg Val Trp Asn Ser Gln Leu Ile
 465 470 475 480
 Arg Tyr Ala Gly Tyr Lys Gln Pro Asp Gly Ser Thr Leu Gly Asp Pro
 485 490 495
 Ala Asn Val Gln Phe Thr Glu Ile Cys Ile Gln Gln Gly Trp Lys Ala
 500 505 510
 Pro Arg Gly Arg Phe Asp Val Leu Pro Leu Leu Leu Gln Ala Asn Gly
 515 520 525
 Asn Asp Pro Glu Leu Phe Gln Ile Pro Pro Glu Leu Val Leu Glu Val
 530 535 540
 Pro Ile Arg His Pro Lys Phe Asp Trp Phe Lys Asp Leu Gly Leu Lys
 545 550 555 560
 Trp Tyr Gly Leu Pro Ala Val Ser Asn Met Leu Leu Glu Ile Gly Gly
 565 570 575
 Leu Glu Phe Ser Ala Cys Pro Phe Ser Gly Trp Tyr Met Gly Thr Glu
 580 585 590
 Ile Gly Val Arg Asp Tyr Cys Asp Asn Ser Arg Tyr Asn Ile Leu Glu
 595 600 605
 Glu Val Ala Lys Lys Met Asp Leu Asp Met Arg Lys Thr Ser Ser Leu
 610 615 620
 Trp Lys Asp Gln Ala Leu Val Glu Ile Asn Ile Ala Val Leu Tyr Ser
 625 630 635 640
 Phe Gln Ser Asp Lys Val Thr Ile Val Asp His His Ser Ala Thr Glu
 645 650 655
 Ser Phe Ile Lys His Met Glu Asn Glu Tyr Arg Cys Arg Gly Gly Cys
 660 665 670
 Pro Ala Asp Trp Val Trp Ile Val Pro Pro Met Ser Gly Ser Ile Thr
 675 680 685
 Pro Val Phe His Gln Glu Met Leu Asn Tyr Arg Leu Thr Pro Ser Phe
 690 695 700

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Glu Tyr Gln Pro Asp Pro Trp Asn Thr His Val Trp Lys Gly Thr Asn
 705 710 715 720
 Gly Thr Pro Thr Lys Arg Arg Ala Ile Gly Phe Lys Lys Leu Ala Glu
 725 730 735
 Ala Val Lys Phe Ser Ala Lys Leu Met Gly Gln Ala Met Ala Lys Arg
 740 745 750
 Val Lys Ala Thr Ile Leu Tyr Ala Thr Glu Thr Gly Lys Ser Gln Ala
 755 760 765
 Tyr Ala Lys Thr Leu Cys Glu Ile Phe Lys His Ala Phe Asp Ala Lys
 770 775 780
 Ala Met Ser Met Glu Glu Tyr Asp Ile Val His Leu Glu His Glu Ala
 785 790 795 800
 Leu Val Leu Val Val Thr Ser Thr Phe Gly Asn Gly Asp Pro Pro Glu
 805 810 815
 Asn Gly Glu Lys Phe Gly Cys Ala Leu Met Glu Met Arg His Pro Asn
 820 825 830
 Ser Val Gln Glu Glu Arg Lys Ser Tyr Lys Val Arg Phe Asn Ser Val
 835 840 845
 Ser Ser Tyr Ser Asp Ser Arg Lys Ser Ser Gly Asp Gly Pro Asp Leu
 850 855 860
 Arg Asp Asn Phe Glu Ser Thr Gly Pro Leu Ala Asn Val Arg Phe Ser
 865 870 875 880
 Val Phe Gly Leu Gly Ser Arg Ala Tyr Pro His Phe Cys Ala Phe Gly
 885 890 895
 His Ala Val Asp Thr Leu Leu Glu Glu Leu Gly Gly Glu Arg Ile Leu
 900 905 910
 Lys Met Arg Glu Gly Asp Glu Leu Cys Gly Gln Glu Glu Ala Phe Arg
 915 920 925
 Thr Trp Ala Lys Lys Val Phe Lys Ala Ala Cys Asp Val Phe Cys Val
 930 935 940
 Gly Asp Asp Val Asn Ile Glu Lys Pro Asn Asn Ser Leu Ile Ser Asn
 945 950 955 960
 Asp Arg Ser Trp Lys Arg Asn Lys Phe Arg Leu Thr Tyr Val Ala Glu
 965 970 975
 Ala Pro Asp Leu Thr Gln Gly Leu Ser Asn Val His Lys Lys Arg Val
 980 985 990
 Ser Ala Ala Arg Leu Leu Ser Arg Gln Asn Leu Gln Ser Pro Lys Phe
 995 1000 1005
 Ser Arg Ser Thr Ile Phe Val Arg Leu His Thr Asn Gly Asn Gln Glu
 1010 1015 1020
 Leu Gln Tyr Gln Pro Gly Asp His Leu Gly Val Phe Pro Gly Asn His
 1025 1030 1035 1040

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Glu Asp Leu Val Asn Ala Leu Ile Glu Arg Leu Glu Asp Ala Pro Pro
 1045 1050 1055
 Ala Asn His Val Val Lys Val Glu Met Leu Glu Glu Arg Asn Thr Ala
 1060 1065 1070
 Leu Gly Val Ile Ser Asn Trp Lys Asp Glu Ser Arg Leu Pro Pro Cys
 1075 1080 1085
 Thr Ile Phe Gln Ala Phe Lys Tyr Tyr Leu Asp Ile Thr Thr Pro Pro
 1090 1095 1100
 Thr Pro Leu Gln Leu Gln Gln Phe Ala Ser Leu Ala Thr Asn Glu Lys
 1105 1110 1115 1120
 Glu Lys Gln Arg Leu Leu Val Leu Ser Lys Gly Leu Gln Glu Tyr Glu
 1125 1130 1135
 Glu Trp Lys Trp Gly Lys Asn Pro Thr Met Val Glu Val Leu Glu Glu
 1140 1145 1150
 Phe Pro Ser Ile Gln Met Pro Ala Thr Leu Leu Leu Thr Gln Leu Ser
 1155 1160 1165
 Leu Leu Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Asp Met Tyr
 1170 1175 1180
 Pro Asp Glu Val His Leu Thr Val Ala Ile Val Ser Tyr His Thr Arg
 1185 1190 1195 1200
 Asp Gly Glu Gly Pro Val His His Gly Val Cys Ser Ser Trp Leu Asn
 1205 1210 1215
 Arg Ile Gln Ala Asp Asp Val Val Pro Cys Phe Val Arg Gly Ala Pro
 1220 1225 1230
 Ser Phe His Leu Pro Arg Asn Pro Gln Val Pro Cys Ile Leu Val Gly
 1235 1240 1245
 Pro Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe Trp Gln Gln Arg Gln
 1250 1255 1260
 Phe Asp Ile Gln His Lys Gly Met Asn Pro Cys Pro Met Val Leu Val
 1265 1270 1275 1280
 Phe Gly Cys Arg Gln Ser Lys Ile Asp His Ile Tyr Arg Glu Glu Thr
 1285 1290 1295
 Leu Gln Ala Lys Asn Lys Gly Val Phe Arg Glu Leu Tyr Thr Ala Tyr
 1300 1305 1310
 Ser Arg Glu Pro Asp Arg Pro Lys Lys Tyr Val Gln Asp Val Leu Gln
 1315 1320 1325
 Glu Gln Leu Ala Glu Ser Val Tyr Arg Ala Leu Lys Glu Gln Gly Gly
 1330 1335 1340
 His Ile Tyr Val Cys Gly Asp Val Thr Met Ala Ala Asp Val Leu Lys
 1345 1350 1355 1360
 Ala Ile Gln Arg Ile Met Thr Gln Gln Gly Lys Leu Ser Glu Glu Asp
 1365 1370 1375

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Ala Gly Val Phe Ile Ser Arg Leu Arg Asp Asp Asn Arg Tyr His Glu
 1380 1385 1390

Asp Ile Phe Gly Val Thr Leu Arg Thr Tyr Glu Val Thr Asn Arg Leu
 1395 1400 1405

Arg Ser Glu Ser Ile Ala Phe Ile Glu Glu Ser Lys Lys Asp Ala Asp
 1410 1415 1420

Glu Val Phe Ser Ser
 1425

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Cys Pro Trp Lys Phe Leu Phe Lys Val Lys Ser Tyr Gln Ser
 1 5 10 15

Asp Leu Lys Glu Glu Lys Asp Ile Asn Asn Asn Val Lys Lys Thr Pro
 20 25 30

Cys Ala Val Leu Ser Pro Thr Ile Gln Asp Asp Pro Lys Ser His Gln
 35 40 45

Asn Gly Ser Pro Gln Leu Leu Thr Gly Thr Ala Gln Asn Val Pro Glu
 50 55 60

Ser Leu Asp Lys Leu His Val Thr Ser Thr Arg Pro Gln Tyr Val Arg
 65 70 75 80

Ile Lys Asn Trp Gly Ser Gly Glu Ile Leu His Asp Thr Leu His His
 85 90 95

Lys Ala Thr Ser Asp Phe Thr Cys Lys Ser Lys Ser Cys Leu Gly Ser
 100 105 110

Ile Met Asn Pro Lys Ser Leu Thr Arg Gly Pro Arg Asp Lys Pro Thr
 115 120 125

Pro Leu Glu Glu Leu Leu Pro His Ala Ile Glu Phe Ile Asn Gln Tyr
 130 135 140

Tyr Gly Ser Phe Lys Glu Ala Lys Ile Glu Glu His Leu Ala Arg Leu
 145 150 155 160

Glu Ala Val Thr Lys Glu Ile Glu Thr Thr Gly Thr Tyr Gln Leu Thr
 165 170 175

Leu Asp Glu Leu Ile Phe Ala Thr Lys Met Ala Trp Arg Asn Ala Pro
 180 185 190

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Arg Cys Ile Gly Arg Ile Gln Trp Ser Asn Leu Gln Val Phe Asp Ala
 195 200 205
 Arg Asn Cys Ser Thr Ala Gln Glu Met Phe Gln His Ile Cys Arg His
 210 215 220
 Ile Leu Tyr Ala Thr Asn Asn Gly Asn Ile Arg Ser Ala Ile Thr Val
 225 230 235 240
 Phe Pro Gln Arg Ser Asp Gly Lys His Asp Phe Arg Leu Trp Asn Ser
 245 250 255
 Gln Leu Ile Arg Tyr Ala Gly Tyr Gln Met Pro Asp Gly Thr Ile Arg
 260 265 270
 Gly Asp Ala Ala Thr Leu Glu Phe Thr Gln Leu Cys Ile Asp Leu Gly
 275 280 285
 Trp Lys Pro Arg Tyr Gly Arg Phe Asp Val Leu Pro Leu Val Leu Gln
 290 295 300
 Ala Asp Gly Gln Asp Pro Glu Val Phe Glu Ile Pro Pro Asp Leu Val
 305 310 315 320
 Leu Glu Val Thr Met Glu His Pro Lys Tyr Glu Trp Phe Gln Glu Leu
 325 330 335
 Gly Leu Lys Trp Tyr Ala Leu Pro Ala Val Ala Asn Met Leu Leu Glu
 340 345 350
 Val Gly Gly Leu Glu Phe Pro Ala Cys Pro Phe Asn Gly Trp Tyr Met
 355 360 365
 Gly Thr Glu Ile Gly Val Arg Asp Phe Cys Asp Thr Gln Arg Tyr Asn
 370 375 380
 Ile Leu Glu Glu Val Gly Arg Arg Met Gly Leu Glu Thr His Thr Leu
 385 390 395 400
 Ala Ser Leu Trp Lys Asp Arg Ala Val Thr Glu Ile Asn Val Ala Val
 405 410 415
 Leu His Ser Phe Gln Lys Gln Asn Val Thr Ile Met Asp His His Thr
 420 425 430
 Ala Ser Glu Ser Phe Met Lys His Met Gln Asn Glu Tyr Arg Ala Arg
 435 440 445
 Gly Gly Cys Pro Ala Asp Trp Ile Trp Leu Val Pro Pro Val Ser Gly
 450 455 460
 Ser Ile Thr Pro Val Phe His Gln Glu Met Leu Asn Tyr Val Leu Ser
 465 470 475 480
 Pro Phe Tyr Tyr Tyr Gln Ile Glu Pro Trp Lys Thr His Ile Trp Gln
 485 490 495
 Asn Glu Lys Leu Arg Pro Arg Arg Arg Glu Ile Arg Phe Arg Val Leu
 500 505 510
 Val Lys Val Val Phe Phe Ala Ser Met Leu Met Arg Lys Val Met Ala
 515 520 525

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Ser Arg Val Arg Ala Thr Val Leu Phe Ala Thr Glu Thr Gly Lys Ser
 530 535 540
 Glu Ala Leu Ala Arg Asp Leu Ala Thr Leu Phe Ser Tyr Ala Phe Asn
 545 550 555 560
 Thr Lys Val Val Cys Met Asp Gln Tyr Lys Ala Ser Thr Leu Glu Glu
 565 570 575
 Glu Gln Leu Leu Leu Val Val Thr Ser Thr Phe Gly Asn Gly Asp Cys
 580 585 590
 Pro Ser Asn Gly Gln Thr Leu Lys Ser Leu Phe Met Leu Arg Glu
 595 600 605
 Leu Asn His Thr Phe Arg Tyr Ala Val Phe Gly Leu Gly Ser Ser Met
 610 615 620
 Tyr Pro Gln Phe Cys Ala Phe Ala His Asp Ile Asp Gln Lys Leu Ser
 625 630 635 640
 His Leu Gly Ala Ser Gln Leu Ala Pro Thr Gly Glu Gly Asp Glu Leu
 645 650 655
 Ser Gly Gln Glu Asp Ala Phe Arg Ser Trp Ala Val Gln Thr Phe Arg
 660 665 670
 Ala Ala Cys Glu Thr Phe Asp Val Arg Ser Lys His His Ile Gln Ile
 675 680 685
 Pro Lys Arg Phe Thr Ser Asn Ala Thr Trp Glu Pro Gln Gln Tyr Arg
 690 695 700
 Leu Ile Gln Ser Pro Glu Pro Leu Asp Leu Asn Arg Ala Leu Ser Ser
 705 710 715 720
 Ile His Ala Lys Asn Val Phe Thr Met Arg Leu Lys Ser Gln Gln Asn
 725 730 735
 Leu Gln Ser Glu Lys Ser Ser Arg Thr Thr Leu Leu Val Gln Leu Thr
 740 745 750
 Phe Glu Gly Ser Arg Gly Pro Ser Tyr Leu Pro Gly Glu His Leu Gly
 755 760 765
 Ile Phe Pro Gly Asn Gln Thr Ala Leu Val Gln Gly Ile Leu Glu Arg
 770 775 780
 Val Val Asp Cys Pro Thr Pro His Gln Thr Val Cys Leu Glu Val Leu
 785 790 795 800
 Asp Glu Ser Gly Ser Tyr Trp Val Lys Asp Lys Arg Leu Pro Pro Cys
 805 810 815
 Ser Leu Ser Gln Ala Leu Thr Tyr Phe Leu Asp Ile Thr Thr Pro Pro
 820 825 830
 Thr Gln Leu Gln Leu His Lys Leu Ala Arg Phe Ala Thr Asp Glu Thr
 835 840 845
 Asp Arg Gln Arg Leu Glu Ala Leu Cys Gln Pro Ser Glu Tyr Asn Asp
 850 855 860

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Trp Lys Phe Ser Asn Asn Pro Thr Phe Leu Glu Val Leu Glu Glu Phe
 865 870 875 880
 Pro Ser Leu His Val Pro Ala Ala Phe Leu Leu Ser Gln Leu Pro Ile
 885 890 895
 Leu Lys Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Gln Asp His Thr Pro
 900 905 910
 Ser Glu Val His Leu Thr Val Ala Val Val Thr Tyr Arg Thr Arg Asp
 915 920 925
 Gly Gln Gly Pro Leu His His Gly Val Cys Ser Thr Trp Ile Arg Asn
 930 935 940
 Leu Lys Pro Gln Asp Pro Val Pro Cys Phe Val Arg Ser Val Ser Gly
 945 950 955 960
 Phe Gln Leu Pro Glu Asp Pro Ser Gln Pro Cys Ile Leu Ile Gly Pro
 965 970 975
 Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe Trp Gln Gln Arg Leu His
 980 985 990
 Asp Ser Gln His Lys Gly Leu Lys Gly Gly Arg Met Ser Leu Val Phe
 995 1000 1005
 Gly Cys Arg His Pro Glu Glu Asp His Leu Tyr Gln Glu Glu Met Gln
 1010 1015 1020
 Glu Met Val Arg Lys Arg Val Leu Phe Gln Val His Thr Gly Tyr Ser
 1025 1030 1035 1040
 Arg Leu Pro Gly Lys Pro Lys Val Tyr Val Gln Asp Ile Leu Gln Lys
 1045 1050 1055
 Gln Leu Ala Asn Glu Val Leu Ser Val Leu His Gly Glu Gln Gly His
 1060 1065 1070
 Leu Tyr Ile Cys Gly Asp Val Arg Met Ala Arg Asp Val Ala Thr Thr
 1075 1080 1085
 Leu Lys Lys Leu Val Ala Thr Lys Leu Asn Leu Ser Glu Glu Gln Val
 1090 1095 1100
 Glu Asp Tyr Phe Phe Gln Leu Lys Ser Gln Lys Arg Tyr His Glu Asp
 1105 1110 1115 1120
 Ile Phe Gly Ala Val Phe Ser Tyr Gly Ala Lys Lys Gly Ser Ala Leu
 1125 1130 1135
 Glu Glu Pro Lys Ala Thr Arg Leu
 1140

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Asp Pro Ala Asn Val Glu Phe Thr Glu Ile Cys Ile Gln Gln Gly
1 5 10 15

Trp Lys Pro Arg
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Asp Pro Met Asn Val Glu Phe Thr Glu Thr Val Ala Leu Lys Met
1 5 10 15

Gln Leu Asp Thr
20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Asp Asn Ser Arg Tyr Asn Ile Leu Glu Glu Val Ala Lys Lys Met
1 5 10 15

Asp Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS :

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly Asp Pro Ala Asn Val Glu Phe Thr Glu Glu Val Ala Lys Lys Met
1 5 10 15
Asp Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGTCTAGATC TATGACTGAA TATGACGTAA TATGACGTAA TGGTACCAGA TCTGGCC

57

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAATGACGTA ACGGAAATGA CGTAACGGAA ATGACGTAAC G

41

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAATGAATTA ACGGAAATGA ATTAACGGAA ATGAATTAAC GG

42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGCACGGGTT TTCGACGTTT ACTGGTAGTG TCTGATGAGG CCGAAAGGCC GAAACGCGAT 60
GCCCATTAACC ACCACGCTCA G 81

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCGACCCACA GTTTCGGGTT TTCGAGCAAG TCTGCTAGTG TCTGATGAGG CCGAAAGGCC 60
GAAACGCGAA GCCGTATTGC ACCACGCTCA TCGAGAAGGC 100

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTAGAGCTTG CAAGCATGCT TGCAAGCAAG CATGCTTGCA AGCATGCTTG CAAGC 55

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCTAGAGCG TACGCAAGCG TACGCAAGCG TACG 34

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Arg Lys Arg Glu Ile Arg Leu Gln Lys Asn Arg Glu Ala Ala Arg Glu
 1 5 10 15

Cys

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAATTCCGTT TTTGAAAAGT GAAGCAATTG AGTGC GGCCC GAAAAAGAGA GCCGCAGAAA	60
GTTTGCGAAC AGAATTTAAT CAAAAACTTG GAGGGTAAAT TGTCCAAGTG GTTCACCTGT	120
TGGCTGCATT TTAAATCAAC GAGGCAAACA ATCAGCGCAG AGGAGCTGCT CCACGTTCCC	180
CGGACAAGAT GTCGCAGCAT TTCACATCGA TATTTGAGAA CCTGCGATTG GTGACCATCA	240
AACGTGCGAC AAATGCGCAA CAGCAACAGC AGCAGCAGCA GCAACAGCAA CTTCAGCAGC	300
AGCAGCAGCA GCTGCAGCAA CAGAAGGCAC AGACACAGCA ACAAATAGC AGAAAAATCA	360
AAACTCAAGC AACGCCAACG TTGAATGGCA ATGGGCTCTT GAGCGGCAAT CCAAATGGCG	420
GAGGCGGTGA CTCCTCGCCC AGCCATGAAG TGGACCATCC GGGTGGAGCA CAAGGAGCTC	480
AAGCAGCAGG AGGCTTGCCA TCTTTAAGTG GCACGCCATT GAGGCACCAC AAGCGCGCCA	540
GTATCTCCAC AGCATCGCCT CCAATTCGCG AACGGCGTGG CACCAACACC AGCATCGTGG	600
TCGAACTGGA TGGCAGTGGC AGCGGGAGTG GGAGTGGCGG TGGTGGCGTT GCGTTTGGTC	660
AGGGTGCGGG TTGTCCTCCC TCGGGCAGCT GCACTGCGTC CGGAAAAAGT TCGCGGGAAC	720
TATCGCCGTC GCCGAAAAAC CAACAGCAGC CCAGAAAGAT GTCACAGGAT TATCGGTGCG	780
GTGCCCGCAG CTTTATGCAC CTGGACGACG AGGGACGCAG TCTGCTGATG CGCAAGCCGA	840

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TGAGACTGAA	GAACATCGAG	GGCAGGCCGG	AGGTCTACGA	CACGCTGCAC	TGCAAGGGTC	900
GCGAGATTCT	TTCCTGCTCG	AAGGCCACCT	GTACGAGCAG	CATTATGAAC	ATTGGCAATG	960
CGGCGGTGGA	GGCCAGGAAA	TCCGATCTGA	TCCTCGAACA	CGCCAAGGAC	TTCCTCGAGC	1020
AGTACTTTAC	ATCGATAAAG	CGTACATCAT	GTACCGCCCA	CGAGACGCGA	TGGAAACAGG	1080
TGCGCCAGAG	CATTGAGACC	ACTGGACACT	ATCAGCTAAC	CGAAACGGAG	CTAATTTATG	1140
GTGCCAAATT	GGCCTGGCGC	AATTCTTCAC	GTTGCATTGG	CCGAATACAA	TGGTCGAAGT	1200
TGCAGGTCTT	TGACTGTCGT	TATGTGACAA	CAACAAGTGG	CATGTTTGAA	GCCATTTGCA	1260
ATCACATTAA	ATATGCAACA	AATAAGGGCA	ACCTGAGATC	GGCCATCACG	ATATTTCCAC	1320
AACGCACAGA	TGCCAAGCAT	GATTATCGCA	TTTGGAAATA	CCAATTAATA	TCTTATGCCG	1380
GCTACAAGCA	GGCGGATGGA	AAAATCATTG	GCGATCCCAT	GAATGTGGAG	TTTACAGAGG	1440
TCTGCACCAA	GCTGGGCTGG	AAGAGCAAGG	GCAGCGAGTG	GGACATACTG	CCATTGGTGG	1500
TCTCGGCCAA	TGGTCACGAT	CCGGACTACT	TTGATTACCC	GCCCGAATTG	ATACTGGAAG	1560
TTCCGCTGAC	CCATCCCAA	TTCGAATGGT	TCTCGGATCT	GGGACTGCGA	TGGTACGCCC	1620
TGCCCCCCGT	ATCCAGTATG	CTGTTTCGATG	TGGGCGGCAT	TCAGTTTACG	GCCACCACAT	1680
TCAGTGGTTG	GTACATGTCTG	ACAGAGATTG	GCAGCCGGAA	TTTATGCGAC	ACAAATCGCC	1740
GCAATATGCT	GGAGACGGTG	GCGCTGAAGA	TGCAACTGGA	CACCCGTACG	CCCACATCCT	1800
TGTGGAAGGA	CAAGGCTGTG	GTGGAGATGA	ACATTGCCGT	GCTCCACTCC	TACCAGAGTC	1860
GCAACGTGAC	CATTGTGGAT	CACCACACGG	CCAGCGAGAG	CTTTATGAAG	CATTTGAGA	1920
ACGAGTCCAA	GCTCAGGAAT	GGGTGTCCCG	CTGATTGGAT	TTGGATCGTG	CCGCCGCTGT	1980
CGGGCTCCAT	AACGCCGGTA	TTCCATCAGG	AGATGGCTCT	GTACTACCTG	AAGCCCTCGT	2040
TCGAGTACCA	GGATCCCGCC	TGGCGAACCC	ACGTGTGGAA	AAAGGGGCGT	GGCGAGAGCA	2100
AGGGCAAGAA	GCCAAGACGT	AAATTCAATT	TTAAACAAAT	CGCTAGGGCT	GTGAAATTTA	2160
CATCGAAACT	ATTTGGACGC	GCCTTATCGA	AACGCATAAA	GGCAACAGTT	CTATATGCCA	2220
CCGAAACTGG	CAAATCGGAG	CAGTATGCGA	AGCAACTTTG	TGAACTCCTA	GGGCACGCAT	2280
TCAATGCACA	GATATATTGC	ATGTCCGACT	ACGATATATC	CTCCATTGAG	CACGAGGCAT	2340
TGTTAATTGT	TGTGGCCTCC	ACCTTTGGCA	ACGGTGATCC	CCCCGAAAAC	GGCGAGCTTT	2400
TCTCCCAGGA	ATTGTATGCG	ATGCGTGTCC	AGGAGTCTTC	CGAGCATGGA	TTGCAGGACT	2460
CCAGCATTGG	CTCGTCAAAG	TCCTTCATGA	AGGCCAGCTC	GCGGCAGGAG	TTCATGAAGC	2520
TGCCACTGCA	ACAGGTGAAG	AGAATCGACC	GATGGGACTC	GCTGCGGGGC	TCCACCTCGG	2580
ACACCTTCAC	CGAGGAGACC	TTTGGTCCCC	TCTCCAATGT	CCGGTTTGCC	GTTTTTGCCC	2640
TCGGCTCCTC	GGCCTATCCA	AATTTCTGCG	CCTTCGGTCA	GSTATGTGGAC	AACATTCTGG	2700

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GCGAGCTGGG	CGGCGAACGC	CTGCTGAGGG	TGGCCTACGG	CGACGAGATG	TGCGGACAGG	2760
AGCAGTCGTT	CCGGAAGTGG	GCGCCCGAGG	TATTCAAGTT	GGCCTGCGAG	ACCTTCTGCC	2820
TGGATCCAGA	GGAGAGCCTT	TCGGATGCCT	CGCTAGCCCT	GCAGAACGAT	TCGCTGACTG	2880
TGAATACGGT	GCGCCTGGTG	CCGTCGGCGA	ATAAGGGATC	CCTGGACAGC	AGTTTATCCA	2940
AGTACCACAA	CAAGAAGGTG	CACTGCTGCA	AGGCGAAGGC	GAAGCCCCAC	AATTTGACCC	3000
GTTTGAGTGA	GGGAGCCAAG	ACAACGATGC	TGCTGGAGAT	CTGTGCACCT	GGCTTGGAGT	3060
ACGAGCCGGG	TGATCATGTG	GGCATCTTTC	CGGCGAATCG	AACGGAACTG	GTCGACGGAC	3120
TGCTAAATCG	ACTGGTGGGT	GTGGATAATC	CCGACGAGGT	GCTGCAGTTG	CAATTGCTAA	3180
AGGAAAAGCA	GACATCGAAT	GGTATATTCA	AGTGCTGGGA	GCCGCACGAC	AAAATACCGC	3240
CGGATACTCT	AAGGAATCTA	CTGGCCCGAT	TCTTTGATCT	GACCACTCCG	CCATCGCGAC	3300
AGCTACTCAC	CCTGCTGGCT	GGATTCTGTG	AGGACACCGC	GGACAAGGAG	CGGCTGGAGT	3360
TGCTGGTCAA	CGATTCTGTC	GCCTACGAGG	ACTGGCGGCA	CTGGCGGCTG	CCGCACCTGC	3420
TGGACGTCCT	CGAGGAGTTC	CCTTCGTGCC	GACCACCGGC	TCCCCTTCTG	CTTGCCCAAC	3480
TAACGCCGCT	GCAGCCTCGC	TTCTATTCCA	TTTCCTCGTC	GCCGCGCCGC	GTTAGTGACG	3540
AAATCCACCT	GACGGTGGCC	ATCGTGAAGT	ACCGTTGTGA	AGATGGTCAG	GGTGACGAGC	3600
GGTACGGCGT	GTGCTCTAAC	TATCTATCCG	GCTTGCGGGC	AGACGACGAG	CTGTTTATGT	3660
TCGTGAGAAG	CGCCTTGGGC	TTCCATTTCG	CCAGCGATCG	GAGTCGTCCC	ATTATTCTGA	3720
TTGGTCCTGG	CACAGGAATA	GCTCCATTCC	GCTCCTTTTG	GCAGGAGTTC	CAGGTGCTAC	3780
GCGACCTTGA	TCCCACGGCC	AAATTGCCCA	AGATGTGGCT	CTTCTTTGGC	TGCCGGAATC	3840
GGGATGTGGA	CTTGACGCC	GAGGAGAAGG	CAGAGCTACA	GAAGGATCAA	ATCCTAGACC	3900
GAGTTTTTCT	CGCTCTGTCC	AGGGAGCAGG	CCATTCCGAA	GACATATGTG	CAGGACCTGA	3960
TTGAGCAGGA	ATTGATTCG	TTGTACCAGT	TGATTGTCCA	GGAGCGGGGC	CACATCTACG	4020
TCTGCGGCGA	TGTCACAATG	GCCGAGCATG	TGTACCAGAC	CATCAGGAAG	TGCATTGCCG	4080
GCAAAGAGCA	GAAAAGCGAG	GCGGAAGTTG	AGACATTTTT	GCTAACACTG	CGGGACGAAA	4140
GTCGCTACCA	CGAGGACATC	TTTGGCATCA	CGCTGCGAAC	GGCTGAGATA	CACACAAAGT	4200
CAAGGGCCAC	GGCCAGGATA	CGAATGGCCT	CCCAGCCCTA	AGGATAGATA	TTCGAAGTAA	4260
TCAAAATAGG	AGGGTGACAT	ATCCAAATTC	GAGAGGAATA	CCAAGCACTT	GCTCTTTTTT	4320
TTCTTCCATA	TTCAAATGCA	ATTAAATATT	GTCGCTTTGT	TCATTACATA	TTCGTATGAA	4380
TAACGTTTAA	ATAAATTACA	TTTTATTATT	GATTCTAATG	TACAAATCAA	TTGTGAAATC	4440
AAAATCTAAA	TGTTAAAATA	TATTTCAAAT	AAACGAATCG	AAAAGGAATT	C	4491

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CLAIMS

What is claimed is:

1. A method of regulating long term memory in an animal comprising inducing of expression of a dCREB2 gene or functional fragment thereof in the animal.
2. The method of Claim 1 wherein the dCREB2 gene encodes a cyclic 3',5'-adenosine monophosphate responsive activator isoform and inducing of said gene results in the potentiation of long term memory.
3. The method of Claim 2 wherein the activator isoform is dCREB2-a or an analogue thereof.
4. The method of Claim 2 wherein induction of the dCREB2 gene encoding a cyclic 3',5'-adenosine monophosphate responsive activator isoform activates the production of a protein which is necessary for the formation of long term memory.
5. The method of Claim 4 wherein the activator isoform is dCREB2-a or an analogue thereof.
6. The method Claim 1 wherein the dCREB2 gene encodes a repressor isoform and inducing of said gene results in the blocking of long term memory.
7. The method of Claim 6 wherein the repressor isoform is dCREB2-b or an analogue thereof.

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8. A method of regulating long term memory in an animal comprising inducing repressor and activator isoforms of dCREB2 wherein long term memory is potentiated in the animal when the net amount of functional activator (ΔC) is greater than zero.
5
9. The method of Claim 8 wherein the repressor isoform is dCREB2-b or an analogue thereof and the activator isoform is dCREB2-a or an analogue thereof.
10. A method of identifying a substance capable of affecting long term memory in an animal comprising the determination that said substance alters the induction or activity of repressor and activator isoforms of dCREB2 from normal in the animal.
10
11. A method of enhancing long term memory formation in an animal comprising increasing the level of activator homodimer from normal in an animal.
15
12. The method of Claim 11 wherein the activator homodimer is a dCREB2a homodimer.
13. A method of enhancing long term memory formation in an animal comprising decreasing the level of activator-repressor heterodimer from normal in an animal.
20
14. The method of Claim 13 wherein the activator-repressor heterodimer is a dCREB2a-dCREB2b heterodimer.
15. A method of enhancing long term memory formation in an animal comprising decreasing the level of repressor homodimer from normal in an animal.
25

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16. The method of Claim 15 wherein the repressor homodimer is a dCREB2b homodimer.
17. A method of identifying a substance capable of affecting long term memory in an animal comprising the determination that said substance alters from normal, in the animal, the formation of a dimer selected from the group consisting of: activator homodimer, activator-repressor heterodimer and repressor homodimer.
18. Isolated DNA encoding a cyclic 3',5'-adenosine monophosphate responsive transcriptional activator.
19. The isolated DNA of Claim 18 wherein the cyclic 3',5'-adenosine monophosphate responsive transcriptional activator is encoded by a *Drosophila* dCREB2 gene.
20. The isolated DNA of Claim 18 wherein the *Drosophila* dCREB2 gene codes for a dCREB2-a isoform.
21. The isolated DNA of Claim 18 which hybridizes to DNA having the sequence in Figure 1A (SEQ ID NO.: 1).
22. The isolated DNA of Claim 18 which encodes the amino acid sequence in Figure 1A (SEQ ID NO.: 2).
23. Isolated DNA encoding an antagonist of cyclic 3',5'-adenosine monophosphate-inducible transcription.
24. The isolated DNA of Claim 23 wherein the antagonist of cyclic 3',5'-adenosine monophosphate-inducible transcription is encoded by a *Drosophila* dCREB2 gene or a functional fragment thereof.

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25. The isolated DNA of Claim 24 wherein the *Drosophila* dCREB2 gene codes for a dCREB2-b isoform.
26. An isolated DNA which encodes a *Drosophila* dCREB2 gene or a functional fragment thereof.
- 5 27. The isolated DNA of Claim 26 wherein the *Drosophila* dCREB2 gene codes for an isoform selected from the group consisting of:
- a) dCREB2-a;
 - b) dCREB2-b;
 - 10 c) dCREB2-c; and
 - d) dCREB2-d.
28. The isolated DNA of Claim 26 wherein the *Drosophila* dCREB2 gene codes for an isoform selected from the group consisting of:
- 15 a) dCREB2-q;
 - b) dCREB2-r; and
 - c) dCREB2-s.
29. Isolated DNA encoding an enhancer-specific activator.
30. The isolated DNA of Claim 29 wherein the enhancer
20 specific activator is encoded by a *Drosophila* dCREB1 gene or a functional fragment thereof.
31. The isolated DNA of Claim 30 which hybridizes to DNA having the sequence in Figure 5 (SEQ ID NO.: 7).
32. The isolated DNA of Claim 30 which encodes the amino
25 acid sequence in Figure 5 (SEQ ID NO.: 8).
33. Isolated DNA encoding a nitric oxide synthase of *Drosophila* (DNOS).

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34. The DNA of Claim 33 encoding a DNOS of neuronal locus.
35. The DNA of Claim 33 encoding a DNOS which contains putative heme, calmodulin, FMN, FAD and NADPH binding site domains.
- 5 36. A method for assessing the effect of a drug on long term memory formation comprising:
- a) administering said drug to *Drosophila*;
 - b) subjecting the *Drosophila* to classical conditioning and to at least one odorant and
10 electrical shock; and
 - c) assessing the performance index of said classical conditioning,
- wherein the effect of said drug occurs when said drug alters said performance index from normal.
- 15 37. A method of Claim 36 wherein said drug affects long term memory formation by altering the induction or activity of repressor and activator isoforms of dCREB2.

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FIGURE 1A

```

1   ATGGACACAGCATCGTCGAGGAGACGGCACTCGTCGGCGGCATCGGGTCCATGAC
1   N D M S I U E E N G N S S A R S G S N D

61  GTGGTCGATGTCGTTGCCACAGCGGGCGGCGGTCGGCGGGCGGGTGGAGGAGGA
21  U U D U U A Q Q A A A A U G G G G G G G

121 GGAGGCGGGCGGGTGGTGGTACCCCGAGCAGCAGACAGAACCCACAAAGTACACG
41  G G G G G G G H P Q Q Q Q Q H P Q S T T

181 GCCGGCGGTCCACGGGTGCGACGACACACGCCAGGGAGGCGGAGTGTCTCCGTGCTG
61  A G G P T G A T H H A Q G G G U S S U L

241 ACCACCCCGCCCACTGCACATACATACCCCATCCAGACGCTGGCGGAGCAGGACTG
81  T T T A M C H I Q Y P I Q T L A Q H G L

301 CAGGTGAGCATTGGGGACCGGGTCTGGTGTCACTGTGAGTGTGAGGTGTACGGA
101 Q U S I U C P G A U C Q L S S U A C V G
      Exon 2

361 TCCAGCCAGAGTGGCTACCAAGGATGTGAGTCCGTGATACAGGCCAATCCCTCGGGA
121 S Q P E U A T K Q U Q S U I Q A N P S G

421 GTCATACAGACAGCAGTGGACCCAGCAGCAGCAGCAGGCGCTGGCCGCCACAGCG
141 U I Q T A R A G T Q Q Q Q Q A L A A A T A

481 ATGCAGAGGTGGTCTACGTGGCCAGCCGCCCACTCGAGGTCATCCACAGACGCT
161 N Q K U U Y U A K P P H S T U I H T T P

541 GGCAATGCAGTGCAGTGCCTACCAAAATCCCTCCACCTTTCATGTAGATCAGGCC
181 G H A U Q U A H K I P P T F P C K I K P
      Exon 4

601 GAACCGAACACGACACCCCGAGGACAGCGACGAGGTCTGTGGACGACGATTCCHU
201 E P H T Q H P E D S D E S L S D D D S Q

661 CACCACCGCAGCGAGCTGACCGGACGGCGTGTACATAGATCTTCCAGGATCAGC
221 H H R S E L T R R P S Y H K I F T E I S
      P-box

721 GGTCCGGACATGAGCGGCGCATCGCTTCCATGTCCGACGGCGTGTCAATCCAGCTG
241 G P D N S G A S L P H S D G U L H S D L
      Exon 6

781 GTGGGGACCGGAGCGGGGGCAATCGCGGACAGCTCCCTGATGCAATTGGATCCACG
261 U G T G A G G H A R H S S L N O L D P T

841 TACTACCTGTCCATCGGATGTCTACACACCAACACAGCGGGATAGCGGAGGATCAG
281 V V L S N A H S Y H T H N S G I A E D Q

901 ACCCGTACGCGGAGATCCGGCTGCAGAGACAGGGAGGCGGCGGTGAGTGCCGCGC
301 T (R)(K)(R)E I (R) L Q (E) H (R) E A (R) E C (R)
      Basic region →

961 AAGAGAGAGGAGTACATCAAGTGCCTGGAGATCGAGTGGCGGTGCTAGAGACCAAAAC
321 (K)(K)(K)E V I (K) C L E N A U A U L E N O N
      Leucine zipper →

1021 AAGCGCTCATCGAGGAGCTGAGTCTGCTCAGGAGCTCTATTGTACGCCAAGACGAT
341 K A L I E E L K S L K E L Y C Q T K H D

1081 TGA
361 END

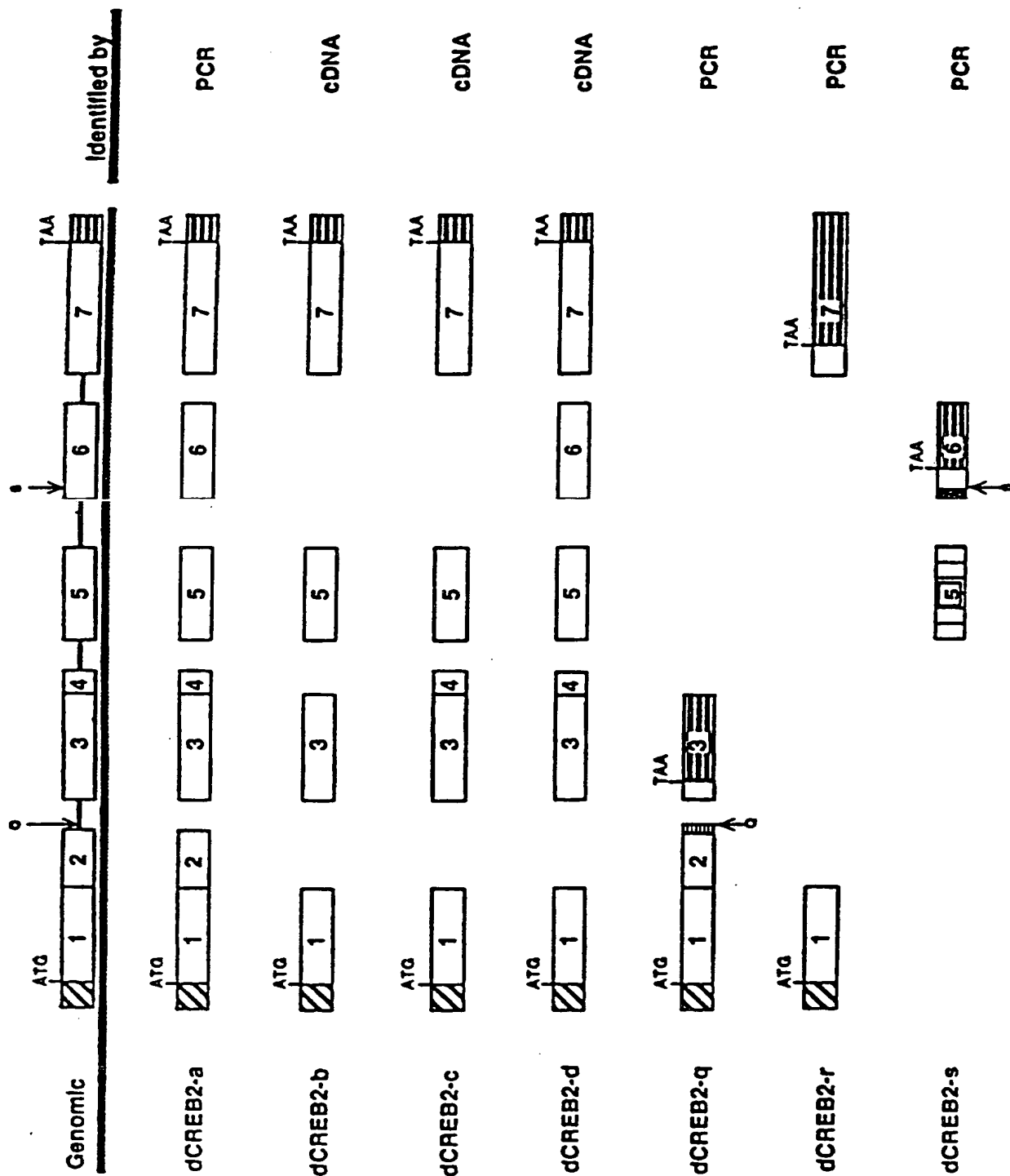
```

FIGURE 1B

```

dCREB2  RKREQLDYHREAAARECAKKKEYD:CLENAUVAULEHONKQIEELQKQYC
CREB    RKREURLMKHREAAARECAKKKEYUKLENAUVAULEHONKTLIEELKALKDLYC
CREM 1  RKRELALMKHREAAARECAKKKEYUKLENAUVAULEHONKTLIEELKALKDLYC
ATF-1   LKREIALMKHREAAARECAKKKEYUKLENAUVAULEHONKTLIEELKTLKOLYS

```



Key: = coding sequences. = 5' untranslated sequences. = 3' untranslated sequences. = intron sequence incorporated by alternative splicing. = coding sequence excluded by alternative splicing. = portion of exon included in spliced transcript is unknown.

Figure 2

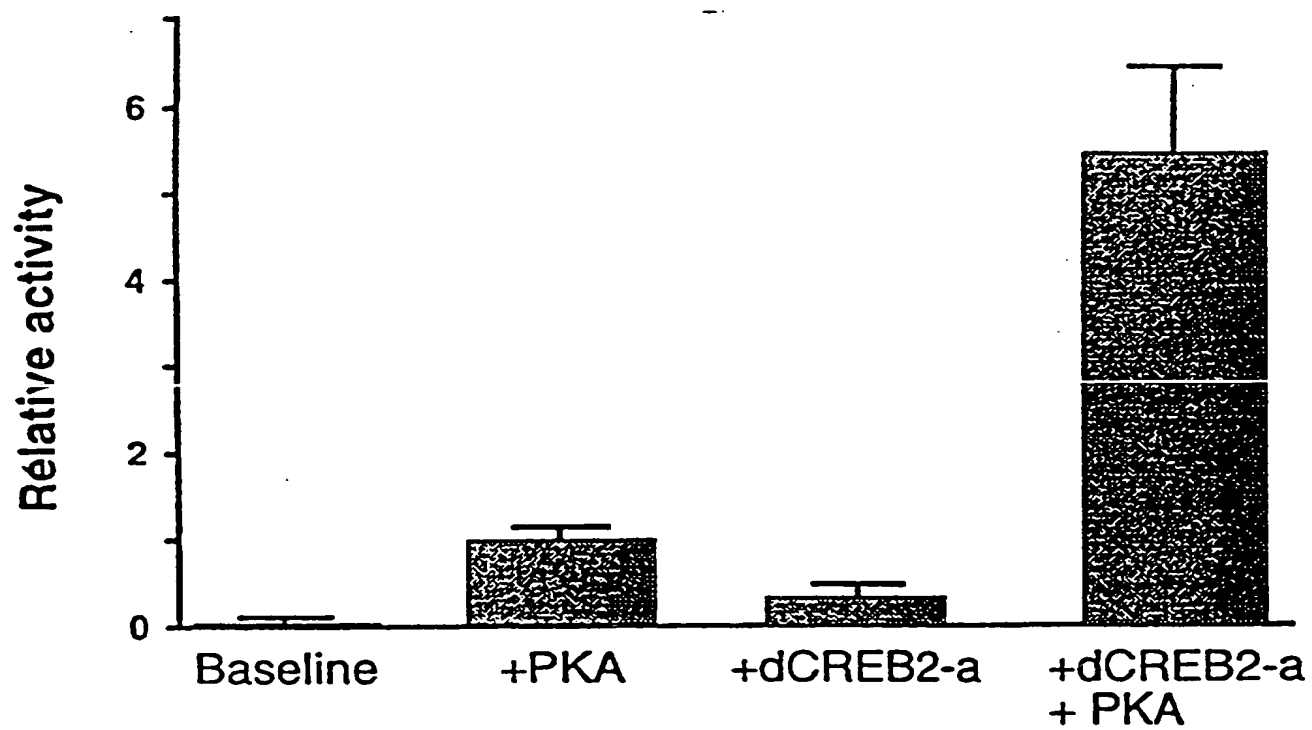


Figure 3

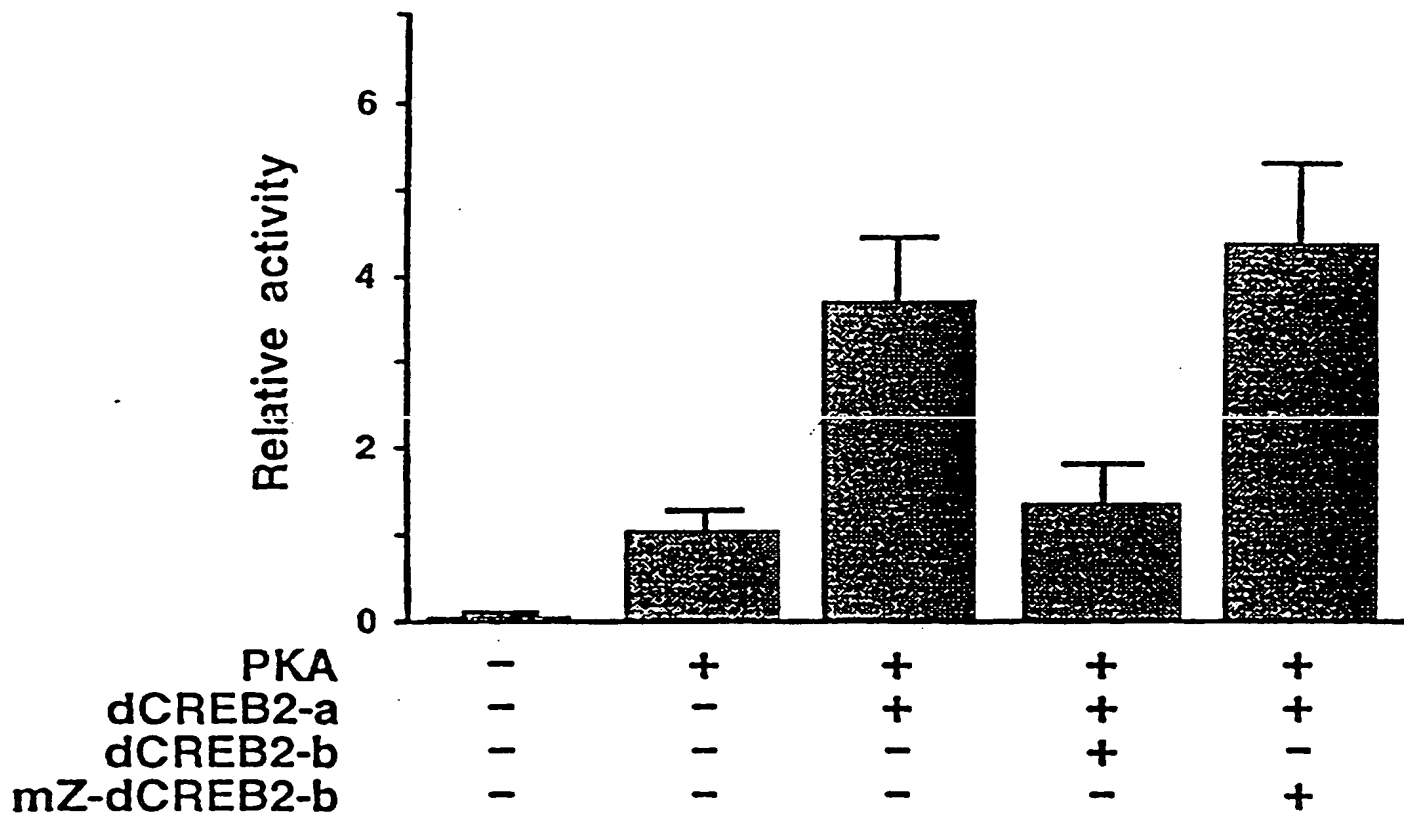


Figure 4

1 ATGTTACTCGGAGAAATATGTTTTCTACTTTACATCGTTAGATGCTGCTACCGCTACA
 1 M L L G E H N F S T F T S L D A A T A T
 61 ACCAACACCGGTGAATTCTTAATGAATGAATCTCCAGGCAAGAGCCGGTGACTTAATG
 21 T H T G E F L N H E S P R Q E A G D L N
 121 TTGGATAGTCTGGATTTCAACATTATCGGCCGAAACCTGGCAGATGATTTCCAGACCTCG
 41 L D S L D F H I N G E H L A D D F Q T S
 181 GCTTACCAGCTTCGGAGGACAAGATGACTCCTTTCTGTTGTTGATACCAATGTTTTGAA
 61 A S P A S E D K N T P F U U D T H U F E
 241 TCCGTCTTCAGAACCCGAGATACCTTCTAGGAGATATCGACATGTTGGTATTGTT
 81 S U F K N T E D T L L G D I D H U G I U
 301 GACACGGAGTTGAAGGAGATGTTGATTTGGTTGACTCGGAATCAATAACGGCACTCCT
 101 D T E L K E N F D L U D S E I H N G T P
 361 ATCAGCAGGAGAGAAAGGATGATTTGGATTTACTTCAAGATCCCAGTCCACCTCAGCT
 121 I K Q E E K D D L E F T S A S Q S T S A
 421 CTCTTGCTCGAATCGACTTCTGCTTCTCCAGCTGATGCTGCCGCTGCATGTGCAAGT
 141 L L S S K S T S A S P A D A R A R C A S
 481 CCTTCGTCTCTCTCTTTGTAAGGATCCTATTCTCTCTCTCAGCTAGAACTACGGGTTGG
 161 P S S S S C K R S Y S S A Q L E T T G S
 541 GATGCTCCAAAGAAAGATAGCTGGGCTGCACCCCTTACACTAGAAACAGAGAAACAAT
 181 D A P K K D K L G C T P V T R K Q R N H
 601 CCATTACCTCCGGTCATTCCAAGGGTCAGGATGTTGCTTCTATGAAAGGGCAGAAAC
 201 P L P P U I P K G Q D U A S N K R A R H
 basic region →
 661 ACTGAGGCGGCAAGAGATCAGAGGCCAGAAAATGGAAGAGATGTCCCACTTGAGGAA
 221 T E A A R R S R A R K N E R N S Q L E E
 Leucine
 721 AAGTGTCAAGCTTGTTCAGGAAACGACGACTTGAAGCTCAAGTTCAAGCTTTGAG
 241 K C Q S L L K E H D D L K A Q U O A L K
 zipper →
 781 AAATTACTTGGACAACAA
 261 K L L G Q Q
 ::::::::::::::::::::::

Figure 5

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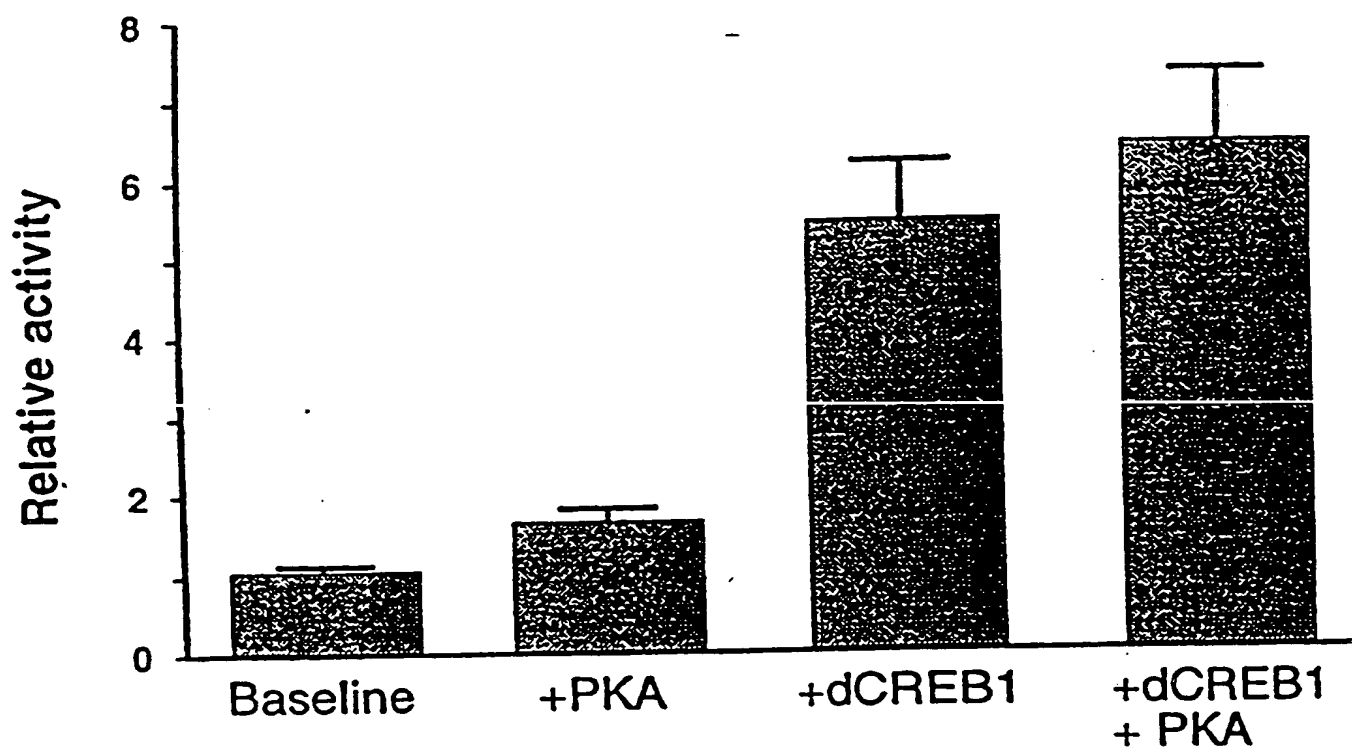


Figure 6

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Figure 7A

LANE #	1	2	3	4	5	6
HEAT SHOCK	-	-	+	+	+3	+3
FLIES	wt	CREB	wt	CREB	wt	CREB

— CREB TRANSGENE
RNA

Figure 7B

LANE #	1	2	3	4	5	6	7	8	9	10	11	12
HEAT SHOCK	-	-	+	+	+1	+1	+3	+3	+9	+9	+24	+24
FLIES	wt	CREB	wt	CREB	wt	CREB	wt	CREB	wt	CREB	wt	CREB

— δ CREB 26
PROTEIN

Figure 7C

lane	1	2	3	4	5	6	7	8
blocker	wt	m	wt	m	wt	m	wt	m
hs	-	-	+	+	+3	+3	+6	+6



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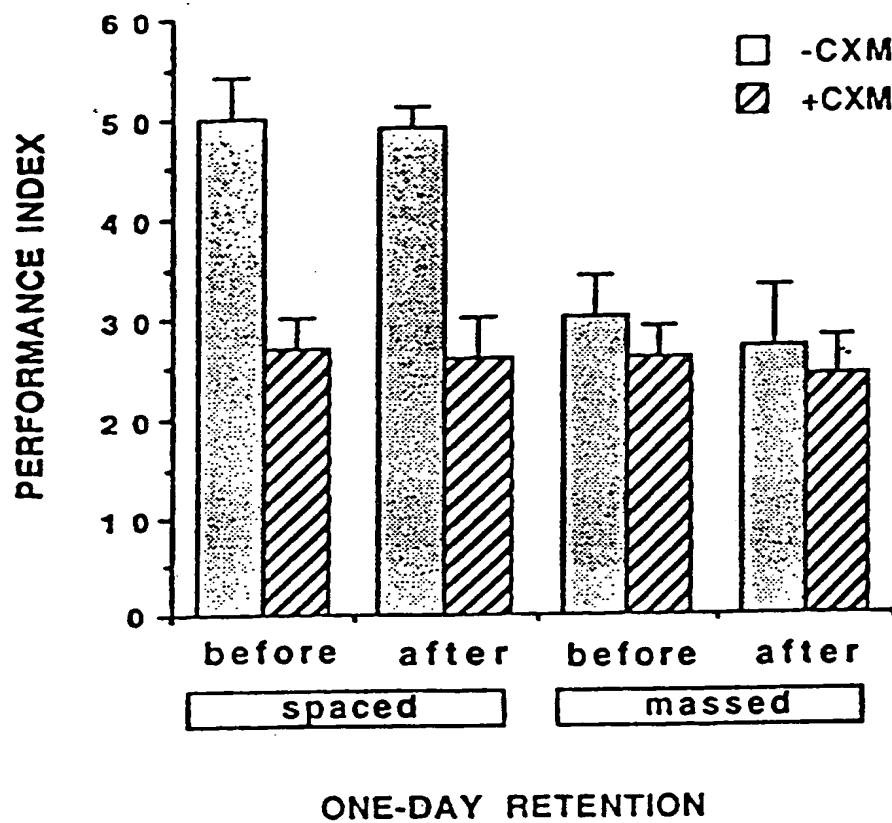


Figure 8

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Figure 9A

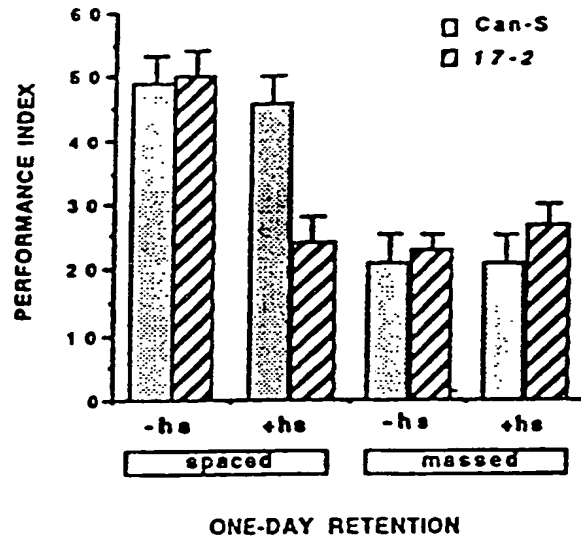


Figure 9B

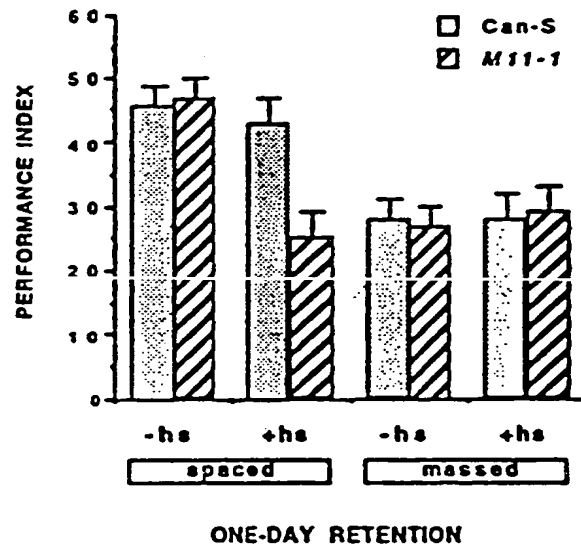
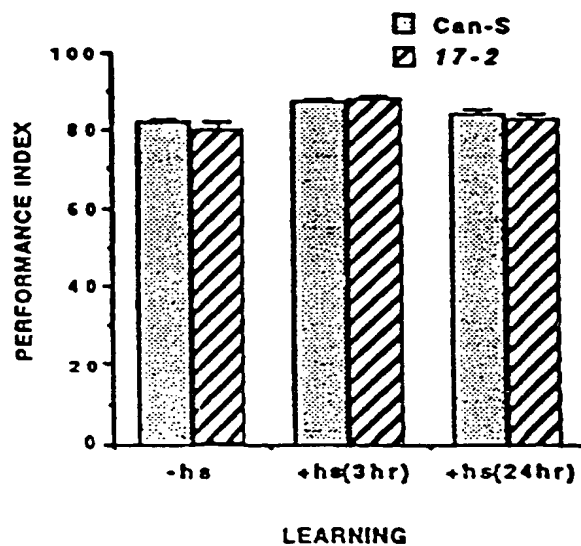


Figure 9C



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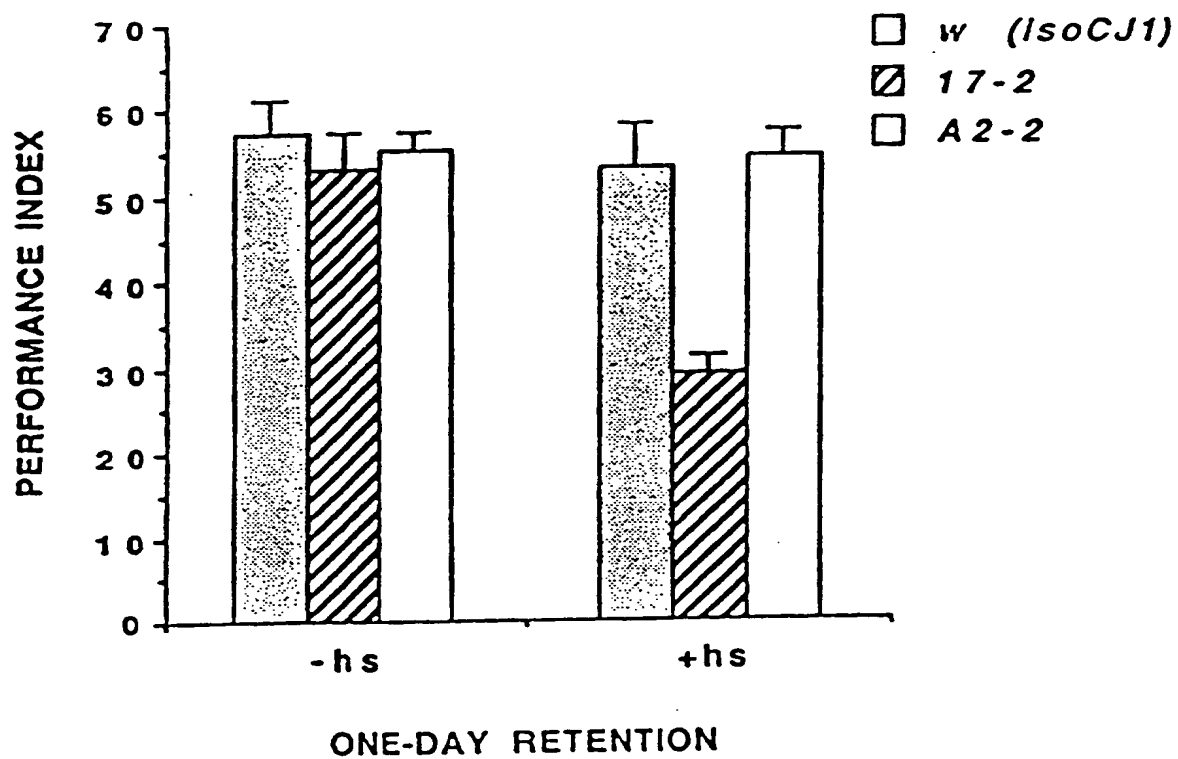


Figure 10

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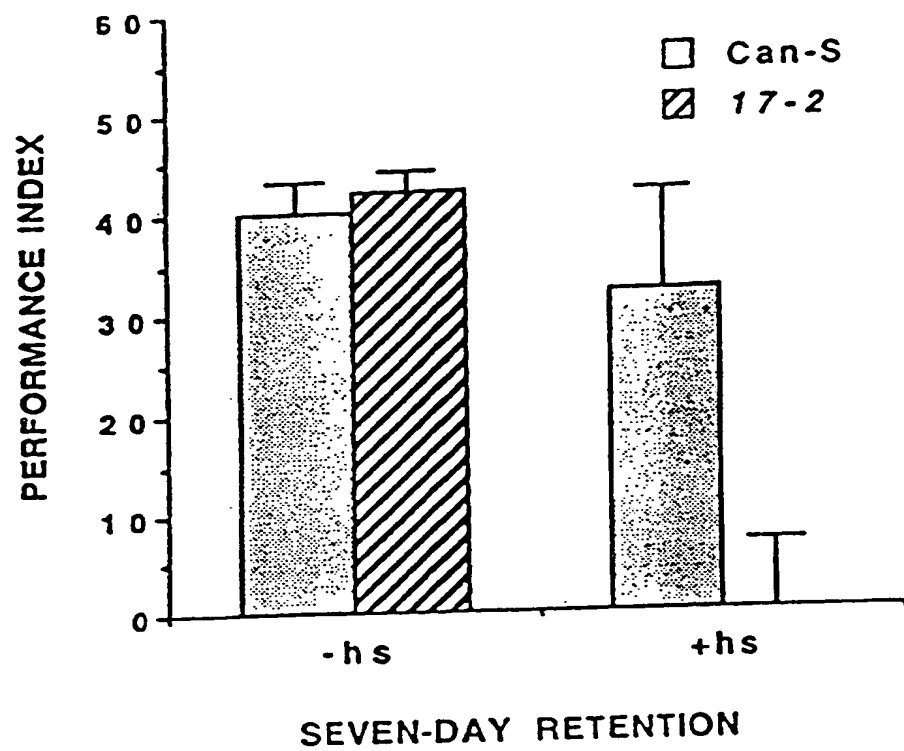


Figure 11

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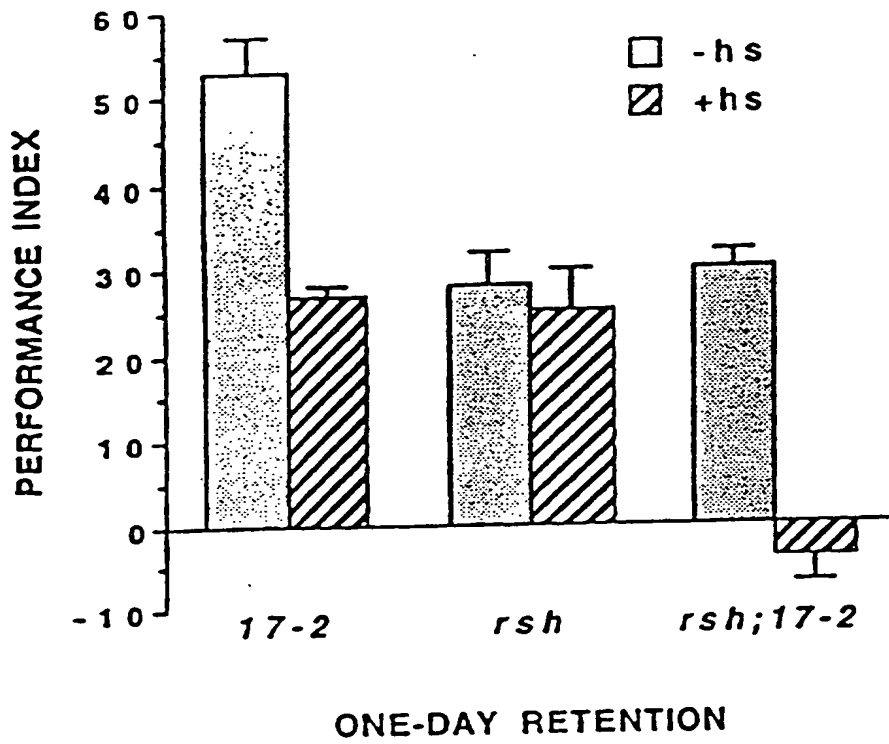


Figure 12

Figure 13A

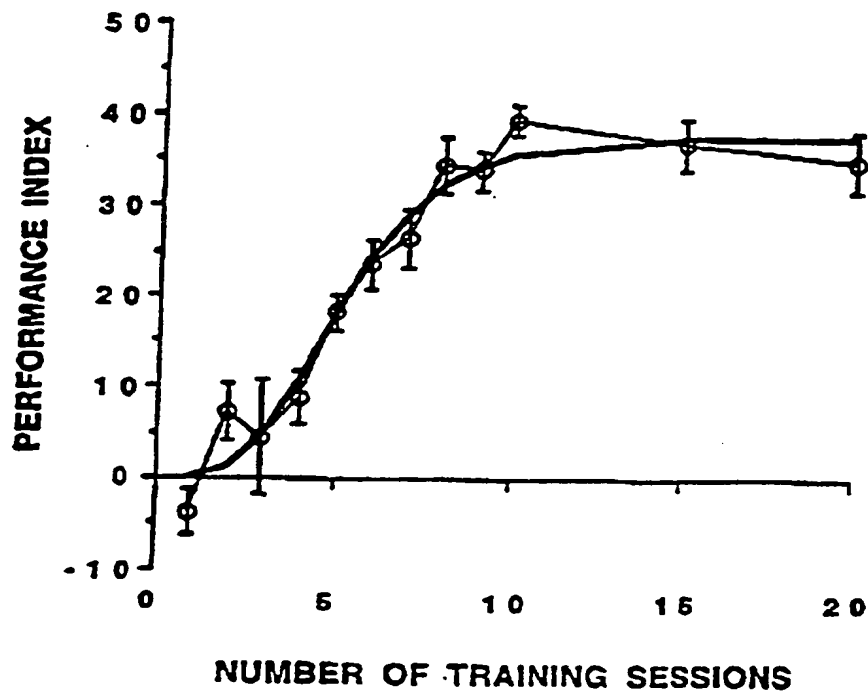
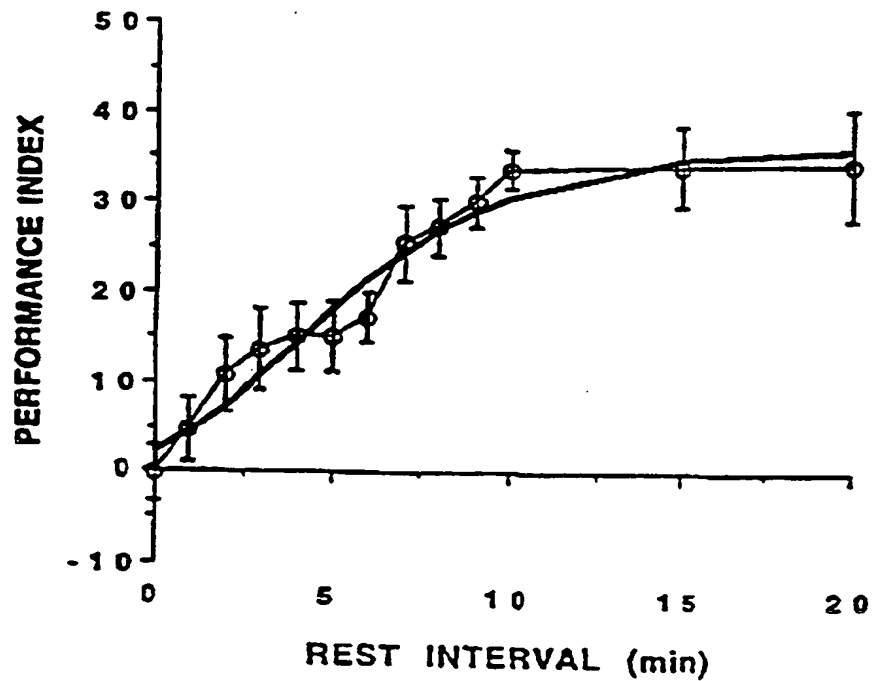


Figure 13B



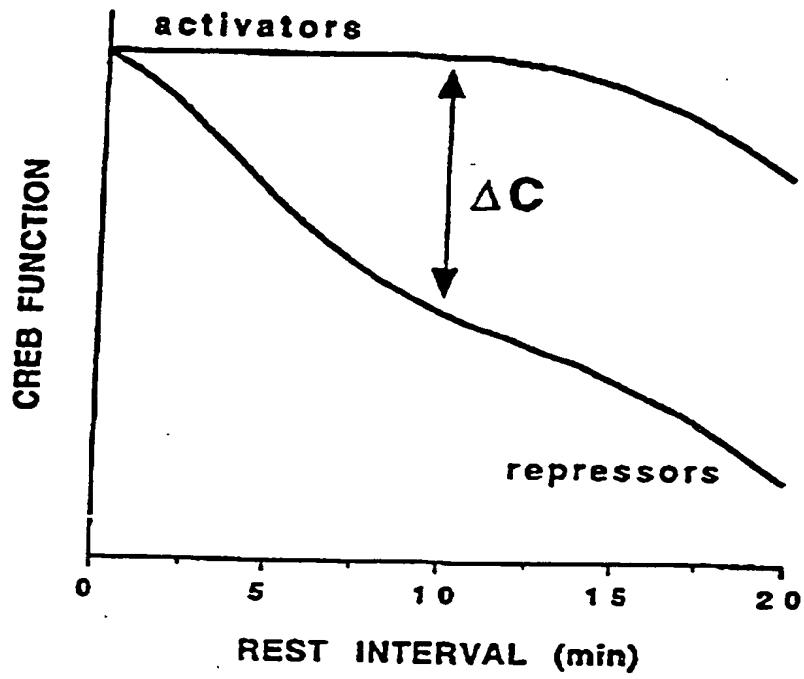


Figure 14

Figure 15A

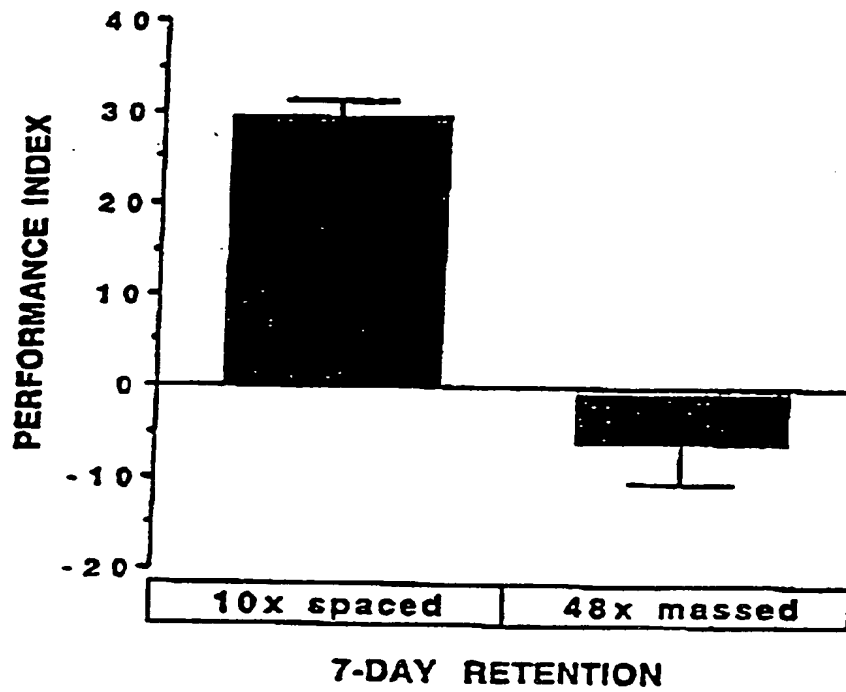
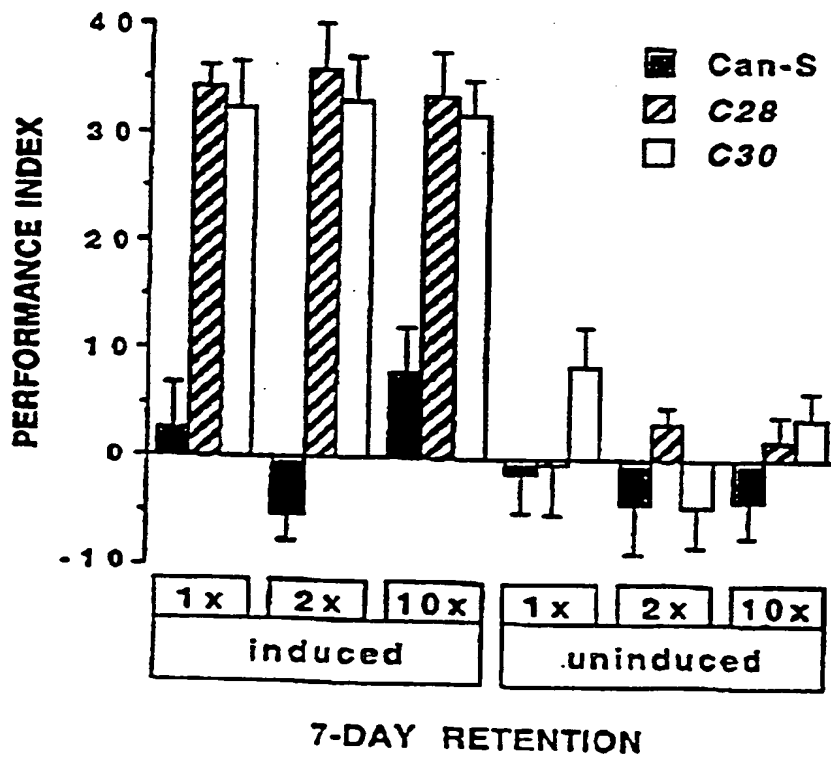


Figure 15B



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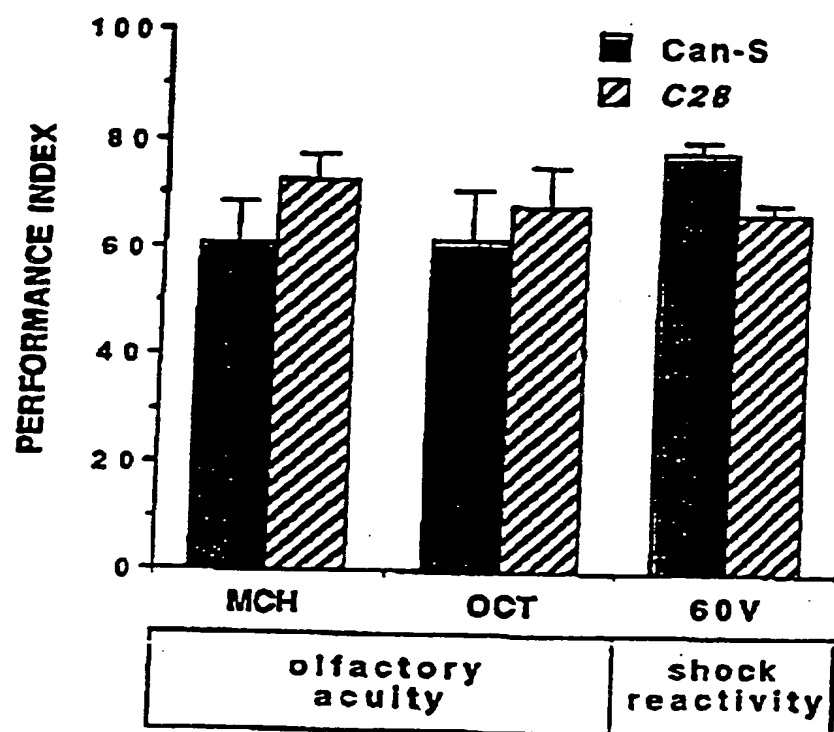


Figure 15C

DNOS	MSQ-----H	FTSIFENLRF	VTIKRATNAQ	QOOOQOQOQO	L-----	35
BENOS	MGN-----	-----L	--KSVG----	--QE--PGPP	-----	14
RNNOS	MEENTFGVQQ	IQPNVISVRL	FKRKVGGLGF	LVKERVSKPP	VIISDLIRGC	50
MMNOS	MAC-----	-----PWKFL	FKVKS-----	--QSDLKEEK	-----	22
DNOS	QOOOQOQOQO	-----	-----KAQTO	QONSRIKIKTO	ATPTLNGNGL	70
BENOS	-----CGL	-----	-----C	L-----GLG--	-----LGLCGK	28
RNNOS	AAEQSGLIQA	GDIILAVNDR	PLVDLSYDSA	LEVLRGIASE	THVVLILRGP	100
MMNOS	-----DI	-----	-----N	N-----NVK--	-----KTPCAV	35
DNOS	LS-GNPNGGG	GDSSPSHEVD	HPGGAQGAQ-	-----	-----AAG	101
BENOS	QG-----	-PASPAPEPS	RAPAPATP--	-----	-----	47
RNNOS	EGFTTHLETT	FTGDGTPKTI	RVTQPLGPPT	KAVDLSHQPS	ASKDQSLAVD	150
MMNOS	LS-----	PTIQDDPKSH	QNGSPQLL--	-----	-----	55
DNOS	GLPSLSGTPL	RHH-----	---KRASIST	ASPPIRERRG	-----	131
BENOS	-----HAPD	HS-----	-----	-PAPNS----	-----	58
RNNOS	RVTGLGNGPQ	HAQGHGQCAG	SVSQANGVAI	DPTMKSTKAN	LQDIGEHDEL	200
MMNOS	-----TGTA	QN-----	-----	--VPESL----	-----	66
DNOS	--TNTSIWVE	LDGSGSGSGS	GG-----	GGVGVGQCAG	CPPSGSCTAS	171
BENOS	-----PTLT-	-----	-----	-----R----	-----PPEG	67
RNNOS	LKEIEPVLSI	LNSGSKATNR	GGPAKAEMKD	TGIQVDRDLD	GKSHKAPPLC	250
MMNOS	-----DKLHV	-----	-----	-----	-----TSTR	75
DNOS	GKSSRELSPS	PKNQQQPRXM	SQDYRSR---	-AGSFMHLDD	EGRSLLMRKP	217
BENOS	-----	-----	-----	-----	-----PKF	70
RNNOS	GDNDRVFNDL	WGKDNVPVIL	NNPYSEKEQS	PTSGKQSPTK	NGSPSRCPRF	300
MMNOS	-----	-----	-----	-----	-----PQY	78
DNOS	HRLKNIEGRF	EYDYLHCKG	REILCCSKAT	CTESTIM---	-IGNAAVEAP	263
BENOS	PRVKNWELGS	ITYDTLCAQS	QQDGPCTPRR	CLGSLVLPK	LQTRPSPGPP	120
RNNOS	LKVKNWETDV	VLTDTLHLKS	TLETGCTEHI	CMGSIMLPSQ	-HTRKPEDVR	349
MMNOS	VRIKNWGSGE	ILHDTLHKA	TSDFTCCKSKS	CLGSIMNPKS	LTRGPRDKPT	128
DNOS	KSDLILEHAK	DFLEQYFTSI	KRTSCTAHET	RWKQVRQSIE	TTGHYQLTET	313
BENOS	PAEQLLSQAR	DFINQYYSI	KRSGSQAHEE	RLQEVEAEVA	STGTIHLRES	170
RNNOS	TKDQLFPLAK	EFLDQYYSI	KRFGSKAHMD	RLEEVNKEIE	STSTYQLKDT	399
MMNOS	PLEELLPHAI	EFINQYGSF	KEAKIEEHLA	RLEAVTKEIE	TTGTYQLTLD	178
-----Heme-----						
DNOS	ELIYGAKLAW	RNSSRCIGRI	QWSKLQVFDC	RYVTTTSGMF	EAICNHIKYA	363
BENOS	ELVFGAKQAW	RNAPRCVGRI	QWGKLQVFDA	RDCSSAQEMF	TYICNHIKYA	220
RNNOS	ELIYGAKHAW	RNASRCVGRI	QWSKLQVFDA	RDCTTAHGME	NYICNHVKYA	449
MMNOS	ELIFATKMAW	RNAPRCIGRI	QWSNLQVFDA	RNCSTAQEMF	QHICRHILYA	228
DNOS	TNKGNLRSAL	TIFPQRTDAK	HQYRIWNNQL	ISYAGYKQAD	GKIIGDPANV	413
BENOS	TNRGNLRSAL	TVFPQRAPGR	GDFRIWNSQL	VRYAGYRQQD	GSVRGDPANV	270
RNNOS	TNKGNLRSAL	TIFPQRTDGK	HDFRVWNSQL	IRYAGYKQPD	GSTLGDPAHV	499
MMNOS	TWNGNIRSAI	TVFPQRSDGK	HDFRLWNSQL	IRYAGYQMPD	GTIRGDAATL	278
DNOS	EFTEVCTKLG	WKSXGSEWDI	LPLVVSANGH	DPDYFDYPPE	LILEVPLTHP	463
BENOS	EITELCIQHG	WTPGNRFDV	LPLLLQAPDE	APELFVLPPPE	LVLEVPLGAP	320
RNNOS	QFTEICIQQG	WKAPRGRFDV	LPLLLQANGN	DPQLFQIPPE	LVLEVPIRHP	549
MMNOS	EFTQLCIDLG	WKPRYGRFDV	LPLVLQADCQ	DPEVFEIPPD	LVLEVTHMHP	328
DNOS	KFEWFSDLGL	RWYALPAVSS	MLFDVGGIQF	TATTFSGWYM	STEIGSRNLC	513
BENOS	HTGVVRGPGL	RWYALPAVSN	MLLEIGGLEF	SAAPFSGWYM	STEIGTRNLC	370
RNNOS	KFDWFKDLGL	KWYGLPAVSN	MLLEIGGLEF	SACPFSGWYM	GTEIGVRDYC	599
MMNOS	KYEFWQELGL	KWYALPAVAN	MLLEVGGLEF	PACPFNGWYM	GTEIGVRDFC	378

Figure 16A

DNOS	DTNRRNMLET	VALKMLQDTR	TPTSLWKDKA	VVEPNIAVLH	SYQSRNVTIV	563
BENOS	DPHRYNILED	VAVCHDLDTR	TTSSLWKDKA	AVEINLAVLH	SFQLAKVTIV	420
RNNOS	DNSRYNILEE	VAKKMDLDMR	KTSSLWKDQA	LVEINIAVLV	SFQSDKVTIV	649
MMNOS	DTQRYNILEE	VGRRMGLETH	TLASLWKDRA	VTEINVAVLH	SFQKQNVTIM	428
DNOS	DHHTASESFH	KHFENESKLR	NGCPADWIWI	VPPLSGSITP	VFHQEMALYY	613
BENOS	DHHAATVSFH	KHLDNEQKAR	GGCPADWAWI	VPPIYGSLLP	VFHQEMVNYI	470
RNNOS	DHHSATESFI	KHMENEYRCR	GGCPADWVWI	VPPMSGSITP	VFHQEMLNYR	699
MMNOS	DHHTASESFH	KHMONEYRAR	GGCPADWIWL	VPPVSGSITP	VFHQEMLNYV	478
CaM						
DNOS	LKPSFEYQDP	AWRTHVWKKG	RGESKGGKPR	RKFNFQKIAR	AVKFTSKLFG	663
BENOS	LSPAIFYQPD	PWKG---SAT	KGAG---ITR	KK-TFKEVAN	AVKISASLMG	513
RNNOS	LTPSFEYQPD	PWNTHVWKG	NGTP---TKR	RAIGFKKLA	AVKFSAKLMG	746
MMNOS	LSPFYFYQIE	PWKTHIWQNE	KLRP----RR	REIRFRVLVK	VVFFASHLMR	524
DNOS	RALSKRIKAT	VLYATETGKS	EQYAKQLCEL	LGHAFNAQIY	CHSDYDISSI	713
BENOS	TLMAKRVKAT	ILYASETGRA	QSYAQQLGRL	FRKAFDPRVL	CHDEYDVVSL	563
RNNOS	QAMAKRVKAT	ILYATETGKS	QAYAKTLCEI	FKHAFDAKAM	SHEEYDIVHL	796
MMNOS	KVMASRVKAT	VLFATETGKS	EALARDLATL	FSYAFNTKVV	CHDQYKASTL	574
DNOS	EHEALLIIVA	STFGNGDPPE	NGELFSQELY	AMRVQESSEH	GLQDSSIGSS	763
BENOS	EHEALVLVVT	STFGNGDPPE	NGESFAAALM	EMSGPYNS--	---SPRPEQH	608
RNNOS	EHEALVLVVT	STFGNGDPPE	NGEKFGCALM	EMRHP-----	---NSVQEER	838
MMNOS	EEEQLLLVVT	STFGNGDCPS	NGQTLKKS-	-----	-----	603
DNOS	KSFMKASSRQ	EFMKLPLQQV	KRIDRWDSL	GSTSDTFTEE	TFCPLSNVRF	813
BENOS	KSYK---IR-	-FNSVS-CSD	PLVSSWRRKR	KESNT---D	SAGALGTLRF	649
RNNOS	KSYK---VR-	-FNSVS-SYS	DSRKSSGDGP	DLRDNF---E	STGPLANVRF	879
MMNOS	--FM---LR-	-----	-----	ELNH-----	-----TFRY	615
FMN						
DNOS	AVFALGSSAY	PNFCAFGQYV	DNILGELGGE	RLLRVAYGDE	MCCQEESFRK	863
BENOS	CVFGLGSRAY	PHFCAFAFARV	DTRLEELGGE	RLQLQGCGDE	LCCQEEAFRG	699
RNNOS	SVFGLGSRAY	PHFCAFGHAV	DTLLEELGGE	RILKMRGDE	LCCQEEAFRT	929
MMNOS	AVFGLGSSMY	PQFCAFAHDI	DQKLSHLGAS	QLAPTGEDE	LSGQEDAFRS	665
DNOS	WAPEVFKLAC	ETFCLOPEES	--LSDASLAL	QNDSLTVNTV	RLVPSANKGS	911
BENOS	WAKAAFQASC	ETFCVGEEAK	---AAQDIFS	PKRSWKQRQY	RLSAQAEGLQ	747
RNNOS	WAKKVFKAAC	DVFCVGDDVN	IEKPNNSLIS	NDRSWKRNKF	RLTYVAEAPD	979
MMNOS	WAVQTFRAAC	ETFDVRSKJH	--IQIPKRFT	SNATWEPQY	RLIQSPEPLD	713
DNOS	LDSSLSKYHN	KKVHCCKAKA	KPH-NLTRLS	EGAKTTHLLE	ICAPGLEYP	960
BENOS	LLPGLIHVHR	RKMFAQTVLS	VENLQSSKST	RATILVRLDT	ACQEGLOQYQ	797
RNNOS	LTQGLSNVHK	KRVSAARLLS	RQNLQSPKFS	RSTIFVRLHT	NGNQELQYQ	1029
MMNOS	LNRALSSIHA	KNVFTMRLLS	QQNLQSEKSS	RTTLVLQLTF	EGSRGPSYLP	763
-FAD-PPi-						
DNOS	GDHVGIFPAN	RTELVDGLLN	RLVGVDNPDE	VLQLQLLKEK	QTSNGIFKCH	1010
BENOS	GDHIGISAPN	RPGLVEALLS	RVEDPPPTE	SVAVEQL-EK	GSPGGPPPSW	846
RNNOS	GDHLGVFPGN	HEDLVNALIE	RLEDAPFANH	VVKVEMLEER	NTALGVISNW	1079
MMNOS	GEHLGIFPGN	QTALVQGILE	RVVDCPTPHQ	TVCLEVLDES	G-----SYW	807
DNOS	EPHDKIPPD	LRNLLARFFD	LTPPSRQLL	TLLAGFCEDT	ADKERLELLV	1060
BENOS	VRDPRLPCT	VRQALTFELD	ITSPSPRLL	RLSTLAEAP	SEQQELETLS	896
RNNOS	KDESRLPPCT	IFQAFKYLD	ITTPPTPLQL	QQFASLATNE	KEQORLLVLS	1129
MMNOS	VKDKRLPPCS	LSQALTYFLD	ITTPPTQLQL	HKLARFATDE	TORQRLEALQ	857
-FAD-ISO-						
DNOS	NDSSAYEDWR	HWRLPHLLDV	LEEFPSCRPP	APLLLAQLTP	LQPRFYSISS	1110
BENOS	QDPRRYEAWK	LVRCPPTLEV	LEQFPSPALP	APLLLTQLPL	LQPRYYSVSS	946
RNNOS	KGLQEYEAWK	WGNJPTMVEV	LEEFPSIQMP	ATLLLTQLSL	LQPRYYSISS	1179
MMNOS	Q-PSYNDWK	FSJNPTFLEV	LEEFPSLHVT	AFLLSQLPI	LKPRYYSISS	906

Figure 16B

DNOS	SPRRVSDEIH	LTVAIVKYRC	EDGQCDERYG	VCSNYLSGLR	ADDELFMFVR	1160
BENOS	APNAHPGEVH	LTVAVLAYRT	QDGLGPLHYG	VCSTWLSQLK	TGDPVPCFIR	996
RNNOS	SPDMYPDEVH	LTVAIVSYHT	RDGEGPVHHC	VCSSWLNRIQ	ADDVVPCFVR	1229
HNOS	SQDHTPSEVH	LTVAVVYRT	RDGQGPLHHC	VCSTWIRNLK	PQDPVPCFVR	956
-----NADPH-Ribose-----						
DNOS	SALGFHLPD	RSRPIILIGP	GTGIAPFRSF	WQEFQVLRDL	DPTAKLPKMW	1210
BENOS	CAPSFRLLPD	PYVPCILVGP	GTGIAPFRGF	WQE-RLHDIE	SKGLQPHMT	1045
RNNOS	CAPSFHLPN	PQVPCILVGP	GTGIAPFRSF	WQQ-RQFDIQ	HKGMNCPMV	1278
HNOS	SVSGFQLPED	PSQPCILIGP	GTGIAPFRSF	WQQ-RLHDSQ	HKGLKGRMS	1005
-----NADPH-Ade-----						
DNOS	LFFGCRNRDV	D-LYAEKAE	LQKDQILDRV	FLALSREQAI	PKTYVQDLIE	1259
BENOS	LVFGCRCSQL	DHLYRDEVQD	AQERGVEGRV	LTAFSREPDS	PKTYVQDILR	1095
RNNOS	LVFGCRQSKI	DHIYREETLQ	AKNKGVFREL	YTAYSREPDR	PKKYVQDVLO	1328
HNOS	LVFGCRHPEE	DHLYQEEMQE	MVRKRVLFOV	HTGYSRLPGK	PKVYVQDILQ	1055
-----NADPH-Ade-----						
DNOS	QEF-DSLYQL	IVQERGHYV	CGDVTMAENV	YQTIRKCIAG	KEQKSEAEVE	1308
BENOS	TELAAEVHRV	LCLERGHMFV	CGDVTMATSV	LQTVQRILAT	EGDMELDEAG	1145
RNNOS	EQLAESVYRA	LKEQGGHIYV	CGDVTMAADV	LKAIQRIMTQ	QCKLSEEDAG	1378
HNOS	KQLANEVLSV	LHGEQGHLYI	CGDVRHARDV	ATTLLKKLVAT	KLNLSEEQVE	1105
-----NADPH-Ade-----						
DNOS	TFLTLRDES	RYHEDIFGIT	LRTAEI----	--HTKSRATA	RIRMAS----	1348
BENOS	DVIGVLRDQQ	RYHEDIFGLT	LRTQEVTSRI	RTQSFSLQER	HLRGAVPWF	1195
RNNOS	VFISRLRDDN	RYHEDIFGVT	LRTYEVNRL	RSESI AFIEE	SKKDADE-VF	1427
HNOS	DYFFQLKSQK	RYHEDIFGAV	F-SYGA----	-KKGSALLEEP	--KAT-----	1142
-----NADPH-Ade-----						
DNOS	-----QP					1350
BENOS	DPPGPDTPGP					1205
RNNOS	-----SS					1429
HNOS	-----RL					1144

Figure 16C

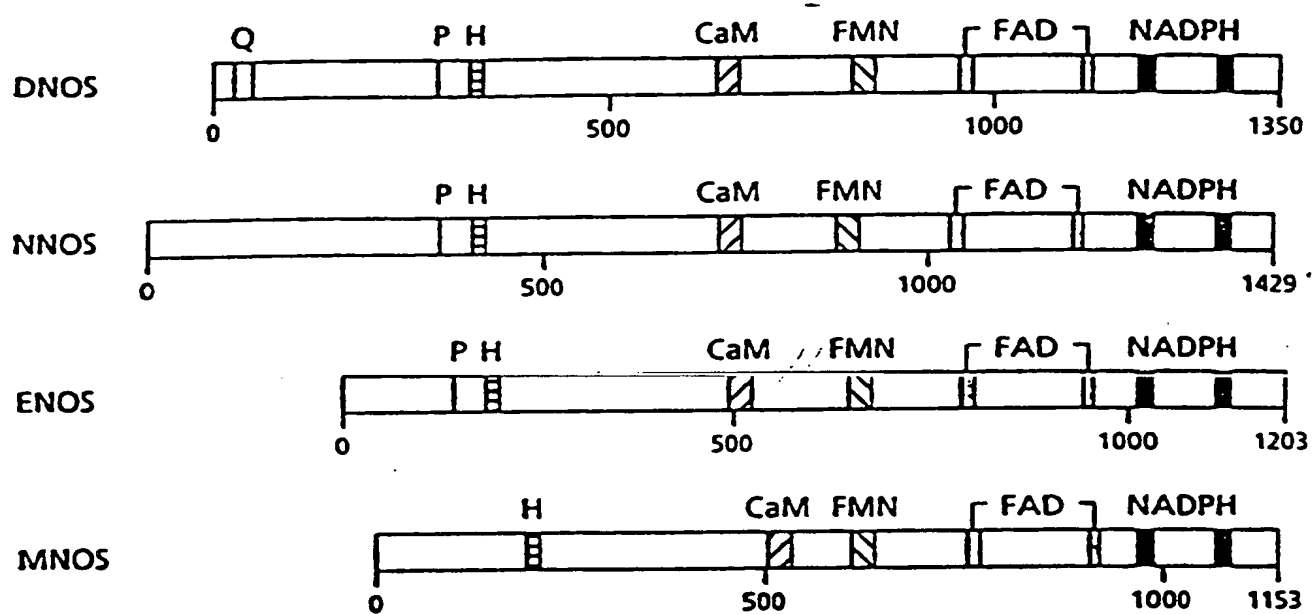


Figure 16D

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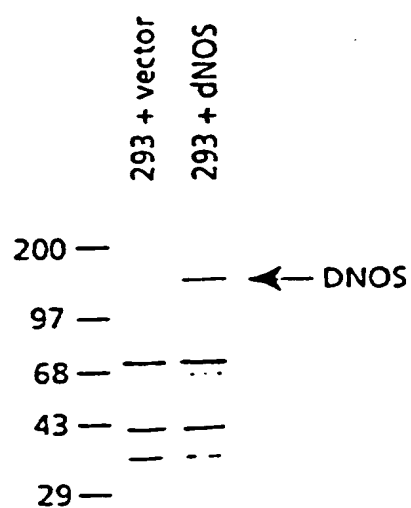


Figure 17A

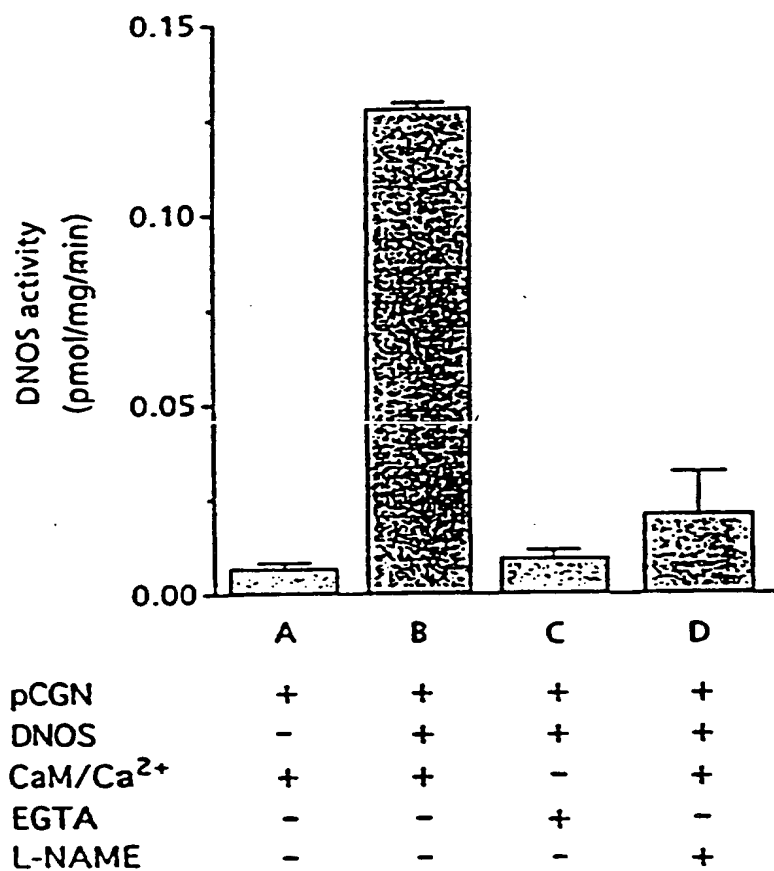


Figure 17B

Sheet 23 of 27

H B

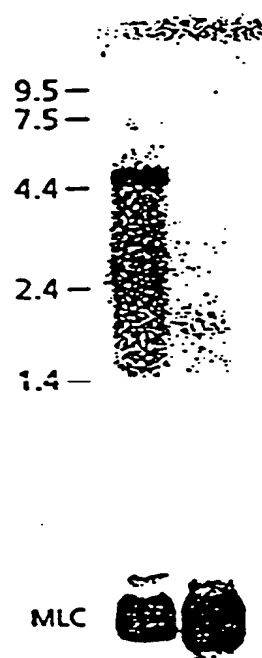


Figure 18A

Sheet 24 of 27

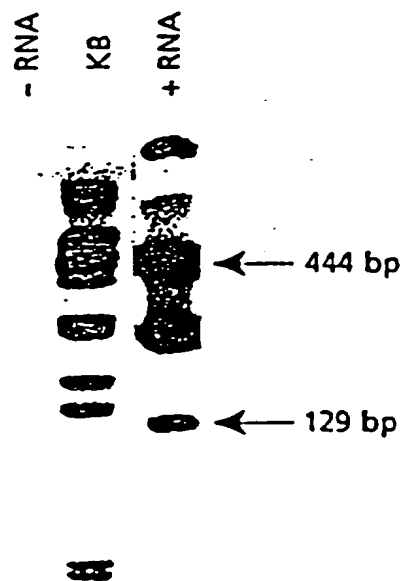


Figure 18B

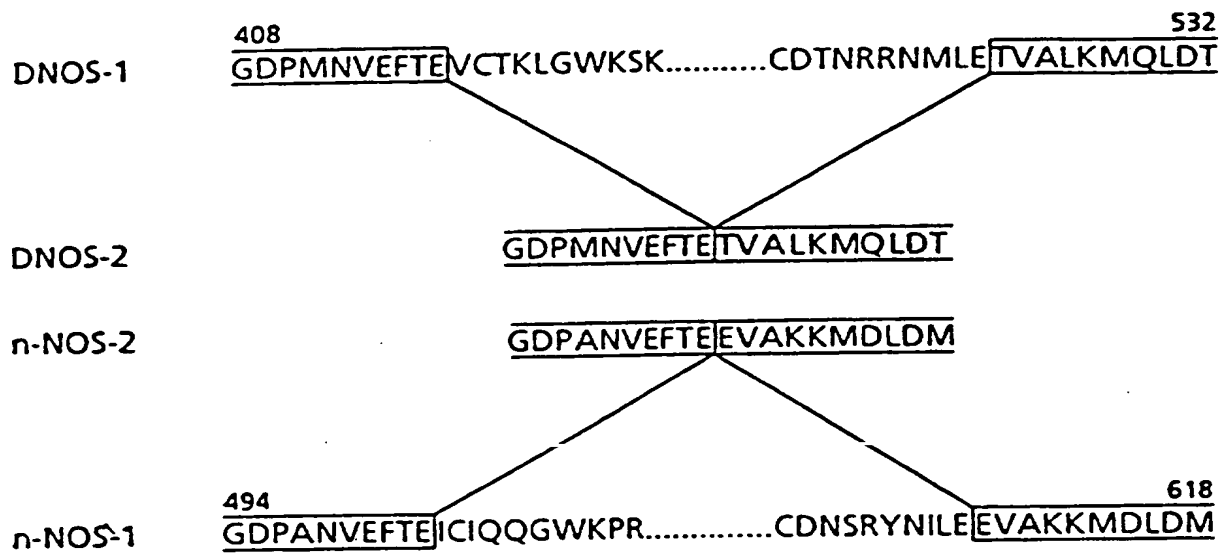


Figure 18C

GAATTCCGTTTTTGAAGCAATTGAGTGCGGCCCGAAAAAGAGAGCCGCA
GAAAGTTTGCGAACAGAATTTAATCAAAAACCTTGGAGGGTAAATTGTCCAAGTGGT
TCACCTGTTGGCTGCATTTTAAATCAACGAGGCAAACAATCAGCGCAGAGGAGCTG
CTCCACGTTCCCCGGACAAGATGTGCGCAGCATTTCACATCGATATTTGAGAACCTGC
GATTCGTGACCATCAAACGTGCGACAAATGCGCAACAGCAACAGCAGCAGCAGCAG
CAACAGCAACTTCAGCAGCAGCAGCAGCAGCTGCAGCAACAGAAGGCACAGACAC
AGCAACAAAATAGCAGAAAAATCAAACTCAAGCAACGCCAACGTTGAATGGCAAT
GGGCTCTTGAGCGGCAATCCAAATGGCGGAGGCGGTGACTCCTCGCCCAGCCATGA
AGTGGACCATCCGGGTGGAGCACAAGGAGCTCAAGCAGCAGGAGGCTTGCCATCTT
TAAGTGGCACGCCATTGAGGCACCACAAGCGCGCCAGTATCTCCACAGCATCGCCTC
CAATTCGCGAACGGCGTGGCACCACACCAGCATCGTGGTTCGAATGGATGGCAGT
GGCAGCGGGAGTGGGAGTGGCGGTGGTGGCGTTGGCGTTGGTCAAGGTGCGGGTTG
TCCTCCCTCGGGCAGCTGCACTGCGTCCGGAAAAAGTTTCGCGGGAACATCGCCGTC
GCCGAAAAACCAACAGCAGCCCAGAAAGATGTCACAGGATTATCGGTGCGGTGCCG
GCAGCTTTATGCACCTGGACGACGAGGACGAGGAGTCTGCTGATGCGCAAGCCGATG
AGACTGAAGAACATCGAGGGCAGGCCGAGGTCTACGACACGCTGCACTGCAAGGG
TCGCGAGATTCTTTCTGCTCGAAGGCCACCTGTACGAGCAGCATTATGAACATTGG
CAATCGCGCGGTGGAGGCCAGGAAATCCGATCTGATCCTCGAACACGCCAAGGACT
TCCTCGAGCAGTACTTTACATCGATAAAGCGTACATCATGTACCGCCACGAGACGC
GATGGAAACAGGTGCGCCAGAGCATTGAGACCACTGGACACTATCAGCTAACCAGAA
ACGGAGCTAATTTATGGTGCCAAATTGGCCTGGCGCAATTCTTCACGTTGCATTGGC
CGAATACAATGGTCGAAGTTGCAGGTCTTTGACTGTCGTTATGTGACAACAACAAGT
GGCATGTTTGAAGCCATTTGCAATCACATTAAATATGCAACAAATAAGGGCAACCTG
AGATCGGCCATCACGATATTTCCACAACGCACAGATGCCAAGCATGATTATCGCATT
TGGAATAACCAATTAATATCTTATGCCGGCTACAAGCAGGCGGATGGAAAAATCAT
TGGCGATCCCATGAATGTGGAGTTTACAGAGGTCTGCACCAAGCTGGGCTGGAAGA
GCAAGGGCAGCGAGTGGGACATACTGCCATTGGTGGTCTCGGCCAATGGTCACGAT
CCGGACTACTTTGATTACCCGCCCGAATTGATACTGGAAGTTCCGCTGACCCATCCC
AAATTCGAATGGTTCTCGGATCTGGGACTGCGATGGTACGCCCTGCCCGCCGTATCC
AGTATGCTGTTTCGATGTGGGCGGCATTGAGTTTACGGCCACCACATTGAGTGGTGG
TACATGTGACAGAGATTGGCAGCCGGAATTTATGCGACACAAATCGCCGCAATAT
GCTGGAGACGGTGGCGCTGAAGATGCAACTGGACACCCGTACGCCACATCCTTGT
GGAAGGACAAGGCTGTGGTGGAGATGAACATTGCCGTGCTCCACTCCTACCAGAGT
CGCAACGTGACCATTTGTGGATCACCAACGCGCCAGCGAGAGCTTTATGAAGCATTTC
GAGAACGAGTCCAAGCTCAGGAATGGGTGTCCCGCTGATTGGATTGATCGTGCC
GCCGCTGTGCGGGCTCCATAACGCCGGTATTCCATCAGGAGATGGCTCTGTACTACCT
GAAGCCCTCGTTTCGAGTACCAGGATCCCGCCTGGCGAACCCACGTGTGAAAAAGG
GGCGTGGCGAGAGCAAGGGCAAGAAGCCAAGACGTAAATTCAATTTTAAACAAATC
GCTAGGGCTGTGAAATTTACATCGAAACTATTTGGACGCGCCTTATCGAAACGCATA
AAGGCAACAGTTCTATATGCCACCGAAACTGGCAAATCGGAGCAGTATGCGAAGCA
ACTTTGTGAACTCCTAGGGCACGCATTCAATGCACAGATATATTGCATGTCCGACTA
CGATATATCCTCCATTGAGCACGAGGCATTGTTAATTGTTGTGGCCTCCACCTTTGGC
AACGGTGTATCCCCCGAAAAACGGCGAGCTTTTCTCCAGGAATTGTATGCGATGCGT
GTCCAGGAGTCTTCCGAGCATGGATTGCAGGACTCCAGCATTGGCTCGTCAAAGTCC
TTCATGAAGGCCAGCTCGCGGCAGGAGTTCATGAAGCTGCCACTGCAACAGGTGAA
GAGAATCGACCGATGGGACTCGCTGCGGGGCTCCACCTCGGACACCTTCACCGAGG
AGACCTTTGGTCCCCTCTCCAATGTCCGTTTGGCGTTTTTGGCCTCGGCTCCTCGGC
CTATCCAAATTTCTGCGCCTTCGGTCAGTATGTGGACAACATTCTGGGCGAGCTGGG
CGGCGAACGCCTGCTGAGGGTGGCCTACGGCGACGAGATGTGCGGACAGGAGCAGT
CGTTCCGGAAGTGGGCGCCCGAGGTATTCAAGTTGGCCTGCGAGACCTTCTGCCTGG
ATCCAGAGGAGAGCCTTTCGGATGCCTCGCTAGCCCTGCAGAACGATTGCTGACTG
TGAATACGGTGGCGCTGGTGGCGTCCGCGAATAAGGGATCCCTGGACAGCAGTTTAT
CCAAGTACCACAACAAGAAGGTGCACTGCTGCAAGGCGAAGGCCGAAGCCCCACAAT
TTGACCCGTTTGAAGTGAGGGAGCCAAGACAACGATGCTGCTGGAGATCTGTGCACCT

Figure 19A

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GGCTTGGAGTACGAGCCGGGTGATCATGTGGGCATCTTTCCGGCGAATCGAACGGA
ACTGGTTCGACGGACTGCTAAATCGACTGGTGGGTGTGGATAATCCCGACGAGGTGC
TGCAGTTGCAATTGCTAAAGGAAAAGCAGACATCGAATGGTATATTCAAGTGCTGG
GAGCCGCACGACAAAATACCGCCGGATACTCTAAGGAATCTACTGGCCCGATTCTTT
GATCTGACCACTCCGCCATCGCGACAGCTACTCACCTGCTGGCTGGATTCTGTGAG
GACACCGCGGACAAGGAGCGGCTGGAGTTGCTGGTCAACGATTCTGTCGGCCTACGA
GGACTGGCGGCACTGGCGGCTGCCGCACCTGCTGGACGTCCTCGAGGAGTTCCCTTC
GTGCCGACCACCGGCTCCCTTTCTGCTTGCCCACTAACGCCGCTGCAGCCTCGCTT
CTATTCCATTTCTCGTCGCCGCGCCGCTTAGTGACGAAATCCACCTGACGGTGGC
CATCGTGAAGTACCGTTGTGAAGATGGTCAGGGTGACGAGCGGTACGGCGTGTGCT
CTAACTATCTATCCGGCTTGCGGGCAGACGACGAGCTGTTTCATGTTCTGTGAGAAGCG
CCTTGGGCTTCCATTTGCCCAGCGATCGGAGTCGTCCCATTTATTCTGATTGGTCCTGG
CACAGGAATAGCTCCATTCCGCTCCTTTTGGCAGGAGTTCCAGGTGCTACGCGACCT
TGATCCACGGCCAAATTGCCCAAGATGTGGCTCTTCTTTGGCTGCCGGAATCGGGA
TGTGGACTTGTACGCCGAGGAGAAGGCAGAGCTACAGAAGGATCAAATCCTAGACC
GAGTTTTTCTCGCTCTGTCCAGGGAGCAGGCCATTCCGAAGACATATGTGCAGGACC
TGATTGAGCAGGAATTCGATTGTTGTACCAAGTTGATTGTCCAGGAGCGGGGCCACA
TCTACGTCTGCGGCGATGTCACAATGGCCGAGCATGTGTACCAGACCATCAGGAAGT
GCATTGCCGGCAAAGAGCAGAAAAGCGAGGCGGAAGTTGAGACATTTTTTGCTAACA
CTGCGGGACGAAAGTCGCTACCACGAGGACATCTTTGGCATCACGCTGCGAACGGC
TGAGATACACACAAAGTCAAGGGCCACGGCCAGGATACGAATGGCCTCCAGCCCT
AAGGATAGATATTCGAAGTAATCAAAATAGGAGGGTGACATATCCAAATTCGAGAG
GAATACCAAGCACTTGCTCTTTTTTTTCTTCCATATTCAAATGCAATTAAATATTGTC
GCTTTGTTCAATTACATATTCGTATGAATAACGTTTAAATAAATTACATTTTATTATTG
ATTCTAATGTACAAATCAATTGTGAAATCAAAATCTAAATGTTAAAATATATTTCAA
ATAAACGAATCGAAAAGGAATTC

Figure 19B

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/13198

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C12N15/53 C07K14/435 C12N9/02 A61K38/17
A61K38/44 G01N33/68 //A01K67/027, C07K16/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DNA AND CELL BIOLOGY, (1993 SEP) 12 (7) 589-95, USUI, T. ET AL. 'Isolation of Drosophila CREB -B: a novel CRE-binding protein.'	26,27
A	see the whole document ---	18-28
X	MOLECULAR AND CELLULAR BIOLOGY, (1992 SEP) 12 (9) 4123-31, SMOLIK, S. ET AL. 'A cyclic AMP-responsive element-binding transcriptional activator in Drosophila melanogaster, dCREB-A, is a member of the leucine zipper family.' see the whole document --- -/-	29

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
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- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
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- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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Date of the actual completion of the international search

21 March 1996

Date of mailing of the international search report

26.03.96

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl,
Fax (+ 31-70) 340-3016

Authorized officer

Andres, S

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
O,X	23RD ANNUAL MEETING OF THE SOCIETY FOR NEUROSCIENCE, WASHINGTON, D.C., USA, NOVEMBER 7-12, 1993. SOCIETY FOR NEUROSCIENCE ABSTRACTS 19 (1-3). 1993. 1066, XP 000566270 TULLY, T. ET AL. 'Independent memories in Drosophila after Pavlovian conditioning.' see abstract ---	36
A	MOLECULAR ENDOCRINOLOGY, vol. 7, no. 2, February 1993 page 145-153 DE GROOT, R. & SASSONE-CORSI, P. 'Hormonal control of gene expression: multiplicity and versatility of cyclic adenosine 3',5'-monophosphate-responsive nuclear regulators' cited in the application see figure 3 ---	1-28
A	EUROPEAN JOURNAL OF NEUROSCIENCE, (1994 AUG 1) 6 (8) 1362-70, MULLER, U. 'Ca ²⁺ /calmodulin-dependent nitric oxide synthase in Apis mellifera and Drosophila melanogaster.' see the whole document ---	33-35
A	SCIENCE, vol. 265, 22 July 1994 US, pages 542-546, O'DELL, T. ET AL. 'endothelial NOS and the blockage of LTP by NOS inhibitors in mice lacking neuronal NOS' cited in the application see the whole document ---	33-36
A	EMBO JOURNAL, vol. 11, 1992 EYNSHAM, OXFORD GB, pages 1503-1512, RUPPERT, S. ET AL. 'Multiple mRNA isoforms of the transcription activator protein CREB: generation by alternative splicing and specific expression in primary spermatocytes' cited in the application see figure 3 ---	1,2,6,28
P,X	CELL, (1994 OCT 7) 79 (1) 49-58, YIN, J. ET AL. 'Induction of a dominant negative CREB transgene specifically blocks long - term memory in Drosophila.' see the whole document --- -/--	1-28,36,37

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/13198

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	CELL, (1995 APR 7) 81 (1) 107-15, YIN, J. ET AL. 'CREB as a memory modulator: induced expression of a dCREB2 activator isoform enhances long - term memory in Drosophila.' see the whole document ---	1-28,36, 37
P,X	MOLECULAR AND CELLULAR BIOLOGY, (1995 SEP) 15 (9) 5123-30, YIN, J. ET AL. 'A Drosophila CREB /CREM homolog encodes multiple isoforms, including a cyclic AMP-dependent protein kinase-responsive transcriptional activator and antagonist.' see the whole document ---	1-28
P,X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1995 SEP 26) 92 (20) 9072-6, REGULSKI, M. ET AL. 'Molecular and biochemical characterization of dNOS: a Drosophila Ca ²⁺ /calmodulin-dependent nitric oxide synthase.' see the whole document -----	33-35

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/13198

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 1-9, 11-16
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 1-9, 11-16 are directed to a method of treatment of (diagnostic method practised on) the human/animal body, the search has been carried out and based on the alleged effects of the compound/ composition.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

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